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(54) Title: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI

(57) Abstract: The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a medicament for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI

Field of the invention

The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

Background to the invention

Invasive fungal infections (e.g. *Candida* spp., *Aspergillus* spp., *Fusarium* spp., *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botritis* spp., Cladosporium spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses, expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is thus an essential element of any new antifungal therapy.

Classical approaches for identifying antifungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic, or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism. These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular target.

Cells from multicellular organisms can commit suicide in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. Cells that are either unwanted or potentially harmful to the organism undergo the apoptotic process and show events like cell shrinkage, chromatin condensation, cytoplasmic condensation, digestion of nuclear DNA, loss of mitochondrial membrane potential, plasma membrane blebbing and phagocytosis of the cell debris (Schwartz, *et al.* 1993). The Bcl-2 family of proteins is centrally involved in the control of the programmed cell death process (PCD). Proteins of this group belong either to the inhibitors of cell death (Bcl-2, Bcl-X_L) or to the group of proteins promoting apoptosis (Bax, Bak) (Oltvai and Korsmeyer 1994; Knudson and Korsmeyer 1997; Reed *et al.* 1998). The ability of the Bcl-2 family of proteins to regulate life and death of a cell is conserved across evolution. Finding of homologues of PCD regulatory genes in plants and animals suggests the possibility that some functions involved in this process may originally have evolved in unicellular organisms, before a divergent development between the plant and the animal kingdom had happened (Apte *et al.* 1995).

Expression of the pro-apoptotic human or mouse Bax protein in *Saccharomyces cerevisiae* did induce cell death in this budding yeast (Sato *et al.* 1994; Greenhalf *et al.* 1996; Zha *et al.* 1996). It was initially described as a process that resembled autophagy with dissolution of the internal organelles and vacuolisation. The apoptotic features characteristic for multicellular eucaryotic cells like morphological changes in nuclear shape and chromatin condensation, were not observed in this yeast (Zha *et al.* 1996). It was therefore suggested that Bax-induced cell death in *S. cerevisiae* is due to the toxicity of the Bax protein itself, mediated by a hypothetical pore-formation without any involvement of a death program (Muchmore *et al.* 1996).

Bax expression in the fission yeast *Schizosaccharomyces pombe* did in contrast show some of the typical apoptotic changes like DNA fragmentation, chromatin condensation, dissolution of the nuclear envelope and cytosolic vacuolisation, suggesting the presence of the evolutionary conserved PCD pathway in this unicellular eucaryote (Ink *et al.* 1997; Jurgensmeier *et al.* 1997). Since it is very unlikely that species dependent differences in the toxicity of the Bax protein are the reason for this observed difference between the two yeasts, a bona fide cell death pathway may well be present in *S. cerevisiae*.

Recent findings of a yeast mutant in the cell division cycle gene *CDC48* show a number of morphological and molecular features that are considered typical indicators of apoptosis markers in metazoan cells: exposure of phosphatidylserine on the outer leaflet of the cytoplasmic membrane, DNA breakage as well as chromatin condensation and fragmentation, supporting the existence of a basic PCD machinery in this unicellular yeast. This theory was

supported by the analysis of a wild type yeast cell expressing the human Bax protein. Comprehensive tests for morphological markers of apoptosis did show a series of changes, identical to morphological markers defining apoptosis (Ligr, Madeo *et al.* 1998). Recent findings from the same group (Madeo *et al.*, 1999) implicate oxygen stress as a general regulator of apoptosis in yeast but the actual mechanism of Bax lethality in *S. cerevisiae* remains unclear.

It is an aim of the present invention to provide new *bax* sequences for expression in yeast and fungi and tools for identifying yeast and candida functions in the pathways leading to programmed cell death.

It is an aim of the present invention to provide nucleic acids as well as polypeptides which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungal infections.

It is a further aim of the present invention to provide uses of these nucleic acid and polypeptide molecules for treating diseases associated with yeast or fungi or for the preparation of (a) medicament(s) for treating said diseases.

It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicament for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds or polypeptides capable of inhibiting or activating expression of the polypeptides of the invention or capable of selectively modulating expression or functionality of such polypeptides. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds or polypeptides.

It is also an aim of the invention to provide methods for preventing infection with yeast or fungi.

It is a further aim of the invention to provide human homologues for the nucleic acids and polypeptides of the invention for use in treating proliferative disorders, such as cancer, or for the prevention of apoptosis in certain diseases, or for the preparation of a medicament for treating such disorders or diseases.

All the aims of the present invention have been met by the embodiments as set out below.

Summary of the invention

Since it has been discovered that the mammalian *bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes. Identification of genes involved in this process could be important for the development of new antifungal therapeutics.

The present inventors overexpressed the Bax protein in the pathogenic yeast *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic *BAX* gene which could be adequately expressed in this pathogenic organism.

Furthermore, the present inventors identified a range of specific nucleic acids which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*. Genes which were differentially expressed (analysed using the Pathways™ software) at different time points after Bax expression are envisaged as candidate genes in the present invention.

Additionally, the invention also relates to *Candida spp.* homologues of the *S. cerevisiae* candidate genes and their uses in stimulating or preventing cell death in yeast and fungi, especially pathogenic yeast and fungi are herewith envisaged.

Furthermore, also part of the invention are the human homologues of these apoptosis-associated *S. cerevisiae* nucleic acids and polypeptides and their potential use in treating proliferative disorders in human and other mammals.

Detailed description of the invention

The present invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248,

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(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614,

616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295,

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(e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and

(g) the complement of any of the nucleic acids as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means the degree of sequence relatedness between two polypeptide or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al*, 1990).

The expression "functional fragment of a nucleic acid" as used herein means the minimal nucleic acid which is necessary to encode a functional protein (or polypeptide). For instance, in situations where a nucleic acid is provided comprising at the 5' end and at the 3' end more nucleotides than the actual open reading frame, the invention also relates to fragments of the nucleic acid which are smaller but which still contain the workable open reading frame. Also meant are parts of the open reading frame encoding a polypeptide having the same properties as the polypeptide encoded by the complete open reading frame.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol.

The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125,

127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713 and 715; from *Candida albicans* are defined in SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 718, 720, 722, 724, 726, 728, 730 and 732.

The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic". Some examples of specific diseases associated with yeast or fungi are further exemplified.

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377,

379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death. According to a more specific embodiment, these nucleic acid sequences are derived from *Aspergillus fumigatus*.

In a more specific embodiment the invention relates to a nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586,

588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731;

(e) a nucleic acid which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NO 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613,

615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and,

(g) the complement of any of the nucleic acids as specified in a) to f).

In a preferred embodiment the invention relates to nucleic acids from *Candida albicans*, as represented by the SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731.

In an even more preferred embodiment the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid corresponds to a mammal or human homologue of at least one of the sequences represented in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657,

659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731.

Therefore, according to a further preferred embodiment, the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid sequence is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;

(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;

(e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;

(f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and

(g) the complement of any of the nucleic acids as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

The invention also relates to the use of said nucleic acids for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.

The expression "proliferative disorders" or "proliferative diseases" refers to an abnormality within a patient or animal such as cancer. Normal cells start to proliferate due to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal benign or malignant mass of tissue is formed that is not inflammatory. Cells of pre-existent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

The expression "apoptosis" or "apoptosis-related diseases" includes diseases such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

It should be clear that the invention also relates to all nucleic acids according to the invention and which are specifically described above, and which can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U. A nucleic acid according to the invention may also comprise any modified nucleotide known in the art.

The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given.

According to the invention, these sequences and their homologues in other yeast and fungi or in human or other mammals as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides. Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., Malassezia spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*, such as, but not limited to:

- Candidiasis, caused by *C. albicans* and other members of the genus Candida, which are primary or secondary mycotic infections, also named candidosis, moniliasis and thrush;
- Aspergilliosis, caused by members of the genus Aspergillus, form a spectrum of diseases;
- Histoplasmosis, caused by *Histoplasma capsulatum*, which is a pulmonary disease always seen in HIV positive or other immunocompromised individuals;
- Paracoccidioidomycosis, caused by *Paracoccidioides brasiliensis*, which is a granulomatous disease that originates as a pulmonary disease;
- Blastomycosis, caused by *Blastomyces dermatitidis*, which may be a benign and self-limiting infection or a chronic granulomatous and suppurative mycosis, also named Chicago disease or Gilchrist's disease;
- Coccidioidomycosis, caused by *Coccidioides imminitis*, and which is a respiratory infection that typically resolves rapidly, but the mycosis can become acute, chronic, severe or fatal; also named San Joaquin Valley fever or Valley fever;
- Cryptococcosis, caused by *Cryptococcus neoformans*, which is a chronic, subacute to acute pulmonary, systemic or meningitic disease, also named Torulosis;

- Sporotrichosis, caused by *Sporothrix schenckii*, which is a chronic infection characterized by nodular lesions of cutaneous or subcutaneous tissues and adjacent lymphatics that suppurate, ulcerate and drain.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore the invention also relates to the potential use of homologous sequences from human or mammalian origin for preventing and/or alleviating diseases or conditions where apoptosis or non-apoptosis of cells is impaired, for instance in proliferative disorders. In this respect also cancer can be seen as a proliferative disorder. Furthermore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art (Sambrook *et al.*, 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous nucleotide sequences.

The present invention further relates to a nucleic acid capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof.

The term "selectively hybridising" or "specifically hybridising" means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions are necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be applied (Sambrook *et al.*, 1989).

As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The invention also relates to an isolated nucleic acid comprising a human homologue of at least one of the yeast or candida nucleic acids described earlier. The invention also relates to a polypeptide encodable by said human homologue of said nucleic acid.

In a further embodiment the invention also relates to an expression vector comprising a human homologue of at least one of the yeast or candida nucleic acids described herein. Said expression vector according can be an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or

eukaryotic host cells. According to a further embodiment, the expression vector comprises an inducible promoter and/or a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

According to a preferred embodiment, the invention relates to an antisense version of any of the nucleic acids of the invention and described above.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid capable of selectively hybridising to at least one of the nucleic acids of the invention. In an interesting embodiment the invention relates to a nucleic acid capable of selectively hybridising to a human homologue of at least one yeast or candida nucleic acid described herein.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

The present invention also advantageously provides nucleic acid molecules of at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically with any of the nucleic acid molecules of the invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene which is desired to be cloned, bringing the primers into

contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P, ^{33}P or ^{35}S, enzyme labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expresssison in host cells, such as a suitable promotor, or the like, to ensure expression of the proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. Said promoter may be either constitutive, inducible or cell- or tissue- or organ-specific. The expression vector may advantageously be a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin, or any other host wherein said vector can be introduced by at least one of the methods known in the art. However, preferred host cells are lower eukaryotic cells such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

In a further embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention further relates to any one of the nucleic acids as defined above for use as a medicament.

Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides,

leading to impaired growth or death of yeast and fungi with reductions of associated illnesses or diseases.

Also envisaged in the present invention are promoter or other control sequences that are comprised within the nucleic acids of the invention, said nucleic acid control sequences can also serve as a target for the identification of compounds or proteins which interfere with the control of expression of downstream encoded polypeptides.

Furthermore, also the human homologues of the yeast and candida nucleic acids may be useful in diseases where apoptosis of cells plays a substantial role, both in situations where apoptosis of (particular) cells is wanted or unwanted.

The invention thus also relates to the use of any of the nucleic acids of the invention or to a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases. As described above, the invention also relates to the use of antisense molecules of the nucleic acids of the invention or to an antisense of any of the human homologues for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.

Said nucleic acids, human homologues and antisense molecules can also be used for the preparation of a medicament for treating or preventing the above-mentioned diseases.

According to yet another embodiment, the invention relates to at least one polypeptide encodable by a nucleic acid of the invention.

The invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

(a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498,

500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54,

56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide

scanning techniques as described in Geysen *et al.* (1986). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75, 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714 and 716. Also according to the invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and the use of human polypeptides as represented by SEQ ID NOs 676, 678, 680, 682, 684 and 686.

Thus, according to a preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of yeast or fungi, for instance a *Candida* spp., selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,

592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and

(d) a functional fragment of any of said polypeptides as defined in a) to c).

According to a further preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of mammalian cells selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs human 676, 678, 680, 682, 684 and 686;

(c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686; and,

(d) a functional fragment of any of said polypeptides as defined in a) to c).

The invention also relates to the polypeptides of the invention and described above for use as a medicament.

Pharmaceutical or fungicidal compositions comprising at least one of the nucleic acids, antisense molecules, polypeptides of the invention optionally together with a pharmaceutically acceptable carrier, diluent or excipient therefor, are also part of the invention.

The polypeptides described above or the human or mammal homologues thereof can also be used for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

The invention furthermore relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof, an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian homologue of said nucleic acid or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative amino acid changes.

The present invention also relates to a vaccine for immunizing a mammal comprising at least one (recombinant) nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier. Preferred vaccines are those that can be used for immunization against infections caused by yeast and fungi. Other preferred vaccines can be used for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions. When a vaccine is used for protecting individuals against certain infections or diseases, it is called a prophylactic vaccine. A vaccine may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

The term "therapeutic" refers to a composition capable of treating infections caused by yeast or fungi or capable of treating proliferative disorders.

Also encompassed within the present invention are antibodies, monoclonal or polyclonal, capable of specifically binding to one or more epitopes of the polypeptides or proteins of the invention. The polypeptides of the invention are represented in SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

The term "specific binding" implies that there is substantially no cross-reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to techniques which are known to those skilled in the art. Monoclonal antibodies may be prepared using conventional hybridoma technology as described by Kohler and Milstein (1979). Polyclonal antibodies may also be prepared using conventional technology well known to those skilled in the art, and which comprises inoculating a host animal, such as a mouse, with a protein or epitope according to the invention and recovering the immune serum. The present invention also includes fragments of whole antibodies which maintain their binding activity, such as for example, Fv, F(ab') and $F(ab')_2$ fragments as well as single chain antibodies.

The antibodies of the invention are capable of specifically binding to at least one of the yeast or candida polypeptides as defined earlier or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue. The invention also relates to the use of said antibodies in treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases. Said antibodies may also be used for the preparation of a medicament for and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.

Antibodies according to the invention may also be used in a method of detecting the presence of a polypeptide according to the invention, which method comprises reacting the antibody with a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi where the yeast or fungus is chosen from, but not restricted to *Candida* spp., Aspergillus spp., Microsporum spp., Trichophyton spp., Fusarium spp., Zygomycetes spp., Botritis, spp., Cladosporium spp., Malassezia spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides imminitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response.

According to another embodiment, the present invention provides a method of identifying compounds or polypeptides which selectively inhibit, induce or interfere with the

expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds (or polypeptides) may carry agonistic or antagonistic properties. The compounds (and polypeptides) to be screened may be of extracellular, intracellular, biologic or chemical origin.

Different alternative methods for identification of said compounds or polypeptides form part of the present invention.

According to a specific embodiment the invention relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences of the invention, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth and/or death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and (e) optionally identifying the compound .

Alternative methods for identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

Another alternative to the above described method comprises (a) contacting a compound to be tested with a genetically modified yeast or fungus in which modification results in the

overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus, in addition to contacting wild type cells with said compound,(b) monitoring the growth and/or death rate and/or activity of said genetically modified yeast or fungi cells compared to said wild type cells wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and, (e) optionally identifying the compound.

The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule of the invention joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound or polypeptide to be tested with at least one of the polypeptides of the invention, (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound or polypeptide being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and (d) optionally identifying the compound or polypeptide.

The invention also relates to a method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of (a) providing a two-hybrid screening system wherein a polypeptide of the invention and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method as described above, are expressed, (b) interacting said compound with the complex formed by the expressed proteins as defined in a), (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and optionally (d) identifying the compound.

According to another embodiment the invention relates to a method for identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises: (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid of the invention joined in frame with a reporter gene, (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and, optionally (c) identifying the compound.

Yet another embodiment of the invention is a method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of: (a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid or by any of the vectors of the invention as a bait and a *S. cerevisiae* cDNA library as a prey are used, (b) detecting an interaction between said polypeptide and a *S. cerevisiae* polypeptide encoded by said cDNA library, and, optionally (c) identifying said *S. cerevisiae* polypeptide.

The term "cells" as used in the above methods relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is measured. Most of these tests comprise following steps: incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scincillation proximity assay) beads are based on the principle that radioactive ^3H can only be measured when present in scincillation fluid. SPA beads contain scincillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scincillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the *GAL4* protein in yeast. Gal4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of Gal4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of Gal4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a *GAL4* transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as ß-galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In addition, compounds active in this test system allow to screen and select compounds which are

able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant progress in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, and even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with ^{15}N or ^{13}C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughout assays or in cases where none of the binding partners are labeled. Other techniques which can be used to study interactions are: overlay, ligand blotting,

band-shift, co-immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein targeting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Yersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing and protein translocation. All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughout assays.

In cases compounds need to be found to target tumor cells, screening assays will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates to *in vitro* and *in vivo* model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. *In vivo* modelsystems allow to test for compound efficacity but also the toxicity of these compounds can be tested. The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Candida* spp., Aspergillus spp., Microsporum spp., Trichophyton spp., Fusarium spp., Zygomycetes spp., Botritis, spp., Cladosporium spp., Malassezia spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides imminitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

The invention also relates to a compound identified using any of the methods of the invention. Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

The invention further relates to a method for preparing pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound as identified above

with a suitable pharmaceutically acceptable carrier. The invention also relates to said pharmaceutical composition.

The compounds or pharmaceutical compositions of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections, more preferably where the yeast or fungus is chosen from *Candida* spp., Aspergillus spp., Microsporum spp., Trichophyton spp., Fusarium spp., Zygomycetes spp., Botritis, spp., Cladosporium spp., Malassezia spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides imminitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

A medicament according to the invention not only relates to fungicidal and fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

According to yet another embodiment, the invention relates to a genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

Also according to the invention is the use of a compound obtainable by a method of the invention, a pharmaceutical composition or a genetically modified organism as described above for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

According to a preferred embodiment, the invention relates to a genetically modified mammalian cell or non-human organism as described above wherein said modification comprises the

expression of an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian homologue of said nucleic acid.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a human homologue thereof and/or at least one of the polypeptides of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

Some examples of preferred human homologues of yeast and/or *Candida* spp. sequences which can be used in the above methods are represented in SEQ ID NOs 675 to 686.

The invention further relates to the compounds identifiable according to the above-described method and their use as a medicament.

The invention further relates to a method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound identifiable according to the above-described methods with a suitable pharmaceutically acceptable carrier.

The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

Furthermore, the present inventors overexpressed the Bax protein in the pathogenic yeast *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic *bax* gene which could be adequately expressed in this pathogenic organism.

Therefore, the present invention relates to an isolated nucleic acid representing a synthetic BAX-gene for expression in *Candida* spp. selected from the group of:

a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,

b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,

c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,

d) a nucleic acid which is more than 75 % identical, preferably more than 80%, 85%, 90% or 95% identical, most preferably more than 97% identical to the nucleic acid as represented by SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c), and

e) a nucleic acid as defined in any one of (a) to (i) interrupted by intervening DNA sequences,

or a nucleic acid representing the complement of any of said nucleic acids as defined in (a) to (d).

The synthetic *BAX* gene shows 73.7% identity with the gene coding for Bax-α. It should be clear that the present invention also relates to nucleic acids wherein other, also frequently used *Candida* spp. codons, are used instead of the choice made for the sequence represented in SEQ ID NO 1. (Table 8)

It should be clear that all nucleic acids according to the invention and which are specifically described above, can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promotor, or the like, to ensure expression of the proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. In this respect, a constitutive or an inducible promoter can be used.

As described in the examples, the invention also relates to nucleic acids and constructs comprising the synthetic *BAX*, or parts thereof, as a fusion with a carrier gene, such as, but not restricted to the yeast *GFP* gene. It is not necessary to include the complete gene of the fusion partner in the expression construct, so the invention relates to various fusion products which can result from the synthetic *BAX* gene and its fusion partner.

The expression vectors comprising the synthetic construct or fusion protein and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin. An interesting host cell according to the invention is a *Candida* spp. cell.

In another embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention also relates to a vector as described above for inducing programmed cell death in *Candida* spp.

The invention further also relates a genetically modified yeast or fungal cell as described above wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

The invention also relates to a genetically modified *Candida* spp. cell wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death

According to a further embodiment, the invention relates to a method for identifying genes in *Candida* spp. which are differentially expressed in a pathway eventually leading to programmed cell death using a synthetic *BAX* gene, as described above, or a vector comprising said gene as described herein, or a genetically modified yeast or fungal cell as described above.

In this respect different model systems are envisaged. It has been shown in the present invention that expression of the synthetic *BAX* gene as a fusion protein more rapidly kills the host cells than when expressed without a fusion partner. Accordingly there will be a difference in which *Candida* spp. genes will be differentially expressed in each system. The invention thus relates to methods for identifying genes in *Candida* spp. which are differentially expressed in a pathway eventually leading to programmed cell death, wherein in said methods the host cells will need a longer or shorter time period for starving. Said time period is dependent on the expression construct or system used.

The invention further relates to a method for obtaining and identifying *Candida* spp. sequences (genes or polypeptides) involved in a pathway eventually leading to programmed cell death comprising the steps of:

a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid as described above or a vector as described above as a bait and a *Candida* spp. cDNA library as a prey are expressed,

b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide encoded by said cDNA library, and,

c) identifying said *Candida* spp. polypeptide.

The invention also relates to a method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:

a) providing a genetically modified organism as described above,

b) expressing a cDNA library in said genetically modified organism, and,

c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.

The invention further relates to a method for identifying Bax-resistant yeast or fungi comprising the steps of:

a) providing (a) genetically modified yeast or fungi as described above,

b) treating said genetically modified yeast or fungi with a mutagen,

c) isolating resistant yeast or fungal cells, and,

d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.

The invention further relates to any of the methods described above wherein said genetically modified organism is a *Candida* spp.

The invention also relates to an isolated *Candida* spp. nucleic acid identifiable by any of the methods described above.

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The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

Figure 1. *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID NOs 17 to 396 and SEQ ID NOs 691 to 716)

Figure 2. *Candida albicans* (SEQ ID NOs 397 to 674, 687, 688 and 717 to 732) and human homologues (SEQ ID NOs 675 to 686).
Human homologues were confirmed via forward and reverse BLAST using BLOSUM62 as a scoring matrix.

YGL080W (SEQ ID NO 161) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (330 bp (SEQ ID NO 675), 109 aa (SEQ ID NO 676)) LOC51660/g7706369 has no reported cellular role or biochemical function.

YGR243W (SEQ ID NO 189) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (384 bp (SEQ ID NO 677), 127 aa (SEQ ID NO 678)) DKFZP564B167/g5817257 has no reported cellular role or biochemical function.

YGR183C (QCR9) (Table 3) codes for a yeast protein with a known cellular role and a known biochemical function. QCR9 codes for subunit 9 of ubiquinol cytochrome-c reductase (7.3 kDa protein) which is a component of the ubiquinol cytochrome-c reductase complex. Cellular role: energy generation.Biochemical function: oxidoreductase and active transporter. The human homologue (132aa (SEQ ID NO 679), 399bp (SEQ ID NO 680)) AF161536 was predicted to have an analogous cellular role and biochemical function.

YBR009C (SEQ ID NO 37), ***YGR209C*** (SEQ ID NO 187) and ***YPR028W*** (SEQ ID NO 393) correspond to known yeast ORFs. Their human homologues have a reported cellular role or biochemical function.

Figure 3. Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters (I and II). Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.
The spots represent the genome wide expression profile without (Minus BAX) and with (Plus BAX) induction of Bax expression for 30 min, 1 hour, 2 hours, 3 hours and 6 hours.

Figure 4 Yeast cells with a disrupted *YGR183C* gene are fully resistant to Bax-induced cell death. Resistance is observed in both the low-copy (A) and the high-copy (B) Bax

expression system. Clonogenic survival was determined by recovering cells at various times from galactose-containing medium and plating of 1000 cells on glucose-based semisolid medium. Data are representative of three experiments (mean ± SD, n=3). SD bars are obscured by symbols.

Figure 5. Scheme for the synthesis of the synthetic *BAX* gene using *C. albicans* optimal codons.

Figure 6. DNA (SEQ ID NO 1) and protein (SEQ ID NO 2) sequence of the synthetic *C. albicans BAX* gene.

Figure 7. Representation of the expression constructs of the synthetic Ca*BAX* gene (A) and the yE*GFP*-synth Ca*BAX* fusion (B).

Figure 8. Growth of the *Candida Albicans* transformants: the individual transformants of pGAL1P:synthCa*BAX* and pGAL1P:*GFP*-synthCa*BAX* were streaked onto plates containing either 2% glucose or 2% galactose as sole carbon source. Growth was monitored 4 days later.

Figure 9. Growth kinetics of GAL1P:synthCa*BAX* (A) and GAL1P:*GFP*-synthCa*BAX* (B) on galactose containing minimal medium.

Figure 10. Immunoblot analysis of two independent transformants of GAL1P:synthCa*BAX* after 15 hours Bax induction on minimal galactose containing media. The arrow at 20kDa indicates the position of the Bax protein. The band seen at 50kDa probably represents a cell wall mannan. Not all of the contamination of the polyclonal Bax antibody could be removed by the threatment with *S. cerevisiae* mannan.

Figure 11. Immunoblot analysis of the GAL1P:*GFP*-synthCa*BAX* strain on galactose containing minimal medium. The band appearing at 45kDa represents the Gfp-Bax fusion protein, while the band at 20kDa represents the Gfp protein alone.

Figure 12. FACS analysis of two independent GAL1P:GFP-synthCa*BAX* transformants grown on galactose containing media: the light grey peak indicates the autofluorescence of the wt strain, the GFP-fluorescence peak is not shaded.

Figure 13. Viability test synthCa*BAX* (A) and GFP-synthCa*BAX* transformants (B): Cells were pregrown in minimal dextrose medium and then switched to fresh minimal medium containing galactose. At the time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represented the viable fraction of the total pool.

Table 1. Oligonucleotides used for construction of the synthetic Ca*BAX*x gene: start and stop codon are in bold, restriction sites used for cloning are in bold and italic.

Tables 2- 6 . Genes modulated by Bax expression in *S. cerevisiae.*
This list includes the genes for which mRNA levels changed significantly after a 30 min (Table 2), 1 hour (Table 3), 2 hours (Table 4), 3 hours (Table 5) or 6 hours (Table 6) induction of Bax protein expression. The Qt values were calculated using the Pathways™ software (Research Genetics).

Table 7. Genes modulated by *Bax* expression in *S. cerevisiae.* This list includes all the genes for which mRNA levels changed significantly after induction of Bax protein exppression. The Qt values were calculated using the Pathways software (Research Genetics). Positive values correspond with upregulated genes. Negative values correspond with downregulated genes. (Comparable with ↑ and ↓respectively in Tables 2-6).

Table 8. Codon usage for the synthetic *BAX* gene.

Table 9. Regulation of 23 selected "Bax-specific" functions.

EXAMPLES

Example 1. Differential gene expression analysis upon Bax-induced cell death

Materials and media

Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was used for the construction and the amplification of plasmids. Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cereviseae* strain INVSc1 (Invitrogen®, San Diego, CA, USA) was transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with YIpUTyL or YIpUTYLMuBax, after linearisation in the Ty δ element (Zhu, 1986).

Cloning of mouse BAX cDNA

Mouse *bax* cDNA, encoding the mouse Bax-α protein, was cloned by Pfu DNA polymerase (Stratagene®, Lo Jolla, CA, USA) chain reaction amplification (PCR) from an EL4/13.18 thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

5'-ATGGACGGGTCCGGGAGCAG-3' (SEQ ID NO 689) and

5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3' (SEQ ID NO 690).

The resulting PCR product was cloned in a *Hin*cII-openend pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).

Plasmid constructions

The 2μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *Cla*I and *Bgl*II. A *Bam*HI-*Hin*dIII *GAL1* promoter fragment was ligated into the *Bgl*II-*Hin*dIII-opened plasmid. A *Xba*I-*Fsp*I *FLP* terminator fragment was inserted into this *Xba*I-*Hin*dIII(blunted)-opened plasmid so that the plasmid YIpUT was obtained. Insertion of a blunted *Eco*RI-*Bsa*AI Ty δ element in the *Kpn*I-*Aat*II-opened and blunted YIpUT resulted in the plasmid YIpUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *Bsa*AI-*Bsr*GI fragment, in the *Bam*HI-openend and blunted YIpUTy resulted in the plasmid YIpUTyL.

Mouse *bax* cDNA was excised from pUC19 by digestion with *Xba*I and *Hin*dIII and subcloned into the *Xba*I-*Hin*dIII-opened plasmid YIpUTyL, obtaining the final expression plasmid YIpUTyLMuBax.

The plasmid YIpUTyLMuBax has been deposited in the BCCM™/LMBP culture collection as pSCTyGALmBax with accession number 3871 under restricted use.

GeneFilters

The Yeast GeneFilters™ were purchased from Research Genetics Inc. (Huntsville, AL, USA).

The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

The yeast filters consist of over 6144 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

Results

Induction of Bax-expression in yeast cells

A preculture of yeast strain INVSc1 containing YIpUTyLMuBax, wherein 5 Bax cassettes under the control of the *GAL1* promotor are integrated in the genome near Ty δ elements, was grown overnight in minimal glucose-containing medium in parallel with the yeast strain INVSc1 containing YIpUTyL as a control. The precultures were diluted in 100-ml minimal glucose-containing medium and grown until an OD_{600} of 1 was reached. Subsequently, the yeast cells were transferred into 100-ml galactose-containing medium and incubated for an additional period of 30 min, 1 hour, 2 hours, 3 hours or 6 hours.

RNA isolation

Total RNA was isolated using RNApure™ Reagent (Genhunter Corporation Nashville, TN, USA) according to the GenHunter protocol. 1.5 10^9 cells were concentrated in a microcentrifuge tube and 1ml RNApure™ Reagent was added together with 1 g of glass pearls. The yeast cells were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA degradation. Chloroform (150 µl) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of Isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA pellet was resuspended in 50 µl RNAse free dH_2O.

First strand cDNA synthesis in the presence of α-^{33}P dCTP

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YIpUTyLMuBax or INVSc1 YIpUTyL yeast cells and incorporation of α-^{33}P dCTP as follows: 2 µl (1 µg/ml) of Oligo dT was added to 20 µg of total RNA in a maximal volume of 8 µl RNase-free dH_2O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

6 µl 5x concentrated First Strand Buffer (GIBCO-BRL, Paisley, UK)

1 µl 0,1 M DTT

1 µl RNase Block (40 units/µl) (Stratagene)

1,5 µl 20 mM dXTP-solution (X = A, G and T) (Amersham Pharmacia biotech Uppsala, Sweden)

1,5 µl SuperScript™ Reverse Transcriptase (200 units/µl) (GIBCO-BRL)

10 µl α-^{33}P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham Pharmacia biotech Uppsala, Sweden),

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Amersham Pharmacia biotech Uppsala, Sweden). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was 5.10^8 cpm/µg for both the INVSc1YIpUTyL and the INVSc1 YIpUTyLMuBax probes.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the S. cerevisiae Yeast GeneFilters™ and signal detection

The Yeast GeneFilters™ were successively hybridised with the α-^{33}P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during hybridisation. The MicroHyb™ solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 5 ml MicroHyb™ solution (42°C) containing 5 µl polydA (1 µg/ml) and incubated for 24 hours at 42°C whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a PhosphorImager™ cassette (Molecular Dynamics, Sunnyvale, CA, USA) with storage phosphor screen. After 4 days of development the screen was scanned at a resolution of 50 µm using the (BioRad, Richmond, CA, USA) Personal FX. The results of these can be seen in Figure 3.

Example 2. Quantification of Hybridisation Signals

Quantification of the hybridisation signals was done using the Pathways™ software (Research Genetics, Huntsville, AL, USA) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. The genes as well as the factors with which they are up- or down- regulated are listed in the Tables 2 to 6 for each individual time point. An overview of the up and down regulated genes modulated in function of induction of Bax expressionfor several time points is shown in Table 7. The sequences of these genes and amino acid sequences that they encode are shown in Figure 1.

Example 3. Comparative gene expression analysis upon Bax-induced cell death and H_2O_2-induced cell death

The oxidative H_2O_2-challenge

A preculture of yeast strain INVSc1 containing YIpUTyL was grown overnight in minimal glucose-containing medium. The preculture was diluted in 100-ml minimal glucose-containing medium and grown until an OD_{600} of 1 was reached. Subsequently, the yeast cells were transferred into 100-ml galactose-containing medium supplemented with 0.1 mM H_2O_2, and

incubated for an additional period of 1 hour. This oxidative challenge resulted in the same final toxicity as a 1-hour induction of Bax expression in the same growth conditions.

First strand cDNA synthesis in the presence of α-^{33}P dCTP

RNA was isolated as mentioned in Example 1. Probes with high specific activity were prepared (detailed in Example 1) by first strand cDNA synthesis using total RNA isolated from INVSc1 YIpUTyLMuBax or INVSc1 YIpUTyL (growth conditions as described in Example 1) or oxidatively stressed INVSc1 YIpUTyL yeast cells.
The specific activity of all probes was 5.10^8 cpm/µg.

Quantification of Hybridisation Signals

Hybridisation and signal detection as described in Example 1. Conversion of the digital images to a 16 bit TIFF format using the Quantity One program (BioRad, Hercules, CA, USA) preserved image data and was necessary for file import into the Pathways® software (Research Genetics, Huntsville, AL, USA). Pathways® was used for the quantification of hybridisation signals and these signals were normalised against all data points.

Identification of Bax-responsive genes

Pairwise comparisons of the normalised data obtained from INVSc1 YIpUTyLMuBax (B) and INVSc1 YIpUTyL (C) revealed differentially expressed genes. To determine the –fold induction or repression, the normalised signal intensity after Bax induction (B) was divided by that before the shock (C). Visual inspection of the hybridisation spots confirmed their selection (*replacement*).

Identification of Bax-specific genes within the Bax-responsive pool

Pairwise comparisons of the normalised data obtained from INVSc1 YIpUTyLMuBax (B) and INVSc1 YIpUTyL (C) at the 1-hour time point revealed differentially expressed genes. Linear ratios (B vs C) were estimated significant when changes were at least two-fold and the normalised signal intensity of one spot was at least tenfold above the average background value. The normalised data of the Bax-responsive genes were compared with data obtained from the H_2O_2-stressed INVSc1 YIpUTyL (H). A Bax-responsive (up-regulated/down-regulated) gene was considered to be Bax-specific when the normalised signal intensity after Bax induction was at least twice as high/low as the corresponding intensity after oxidative stress. Visual inspection of the hybridisation spots confirmed their selection. An overview of the Bax-

specific genes for the 1-hour time point is shown in Table 9. The sequences of these genes and amino acid sequences that they encode are shown in Figure 2.

Example 4. Search for homologues in *Candida albicans* and human

Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).

Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.

The sequences of homologues *Candida* spp. and human genes and the corresponding amino acid sequences are shown in Figure 2.

Example 5. Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans*

The method proposed is based on observations (Sandbaken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to the wild type (WT) cell.

Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component

which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth and/or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti-sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

Example 6. Assay for High Throughput screening for drugs

35 µl minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems, Helsinki, Finland). A 96-channel pipettor transfers 2.5 µl of R-compound at 10^{-3} M in DMSO from a stock plate into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at –70°C. The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C. For the parent strain, CAI-4, the medium is always supplemented with 20 µg/ml uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250.000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20.000 to 50.000 cells/ml. Cultures are grown at 30°C while shaking at 250 rpm until a final OD_{600} of 0.24 (+/- 0.04) is reached.

200 µl of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 µl total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Example 7. Yeast cell viability assay upon induction of Bax expression

Materials and media

Yeast stains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* BY4742 wild type strain and BY4742 with the *YGR183C* gene disruption (EUROSCARF collection) were transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with the low-copy centromeric pRS415Bax plasmid or pRS415 as a control, or with the high-copy episomal pRS425Bax plasmid or pRS425 as a control.

Plasmid constructions

The Bax expression cassette, a *Bsg*I(blunted)-*Sap*I(blunted) fragment excised from YIpUTyLMuBax containing the *GAL1* promoter, the *bax* cDNA and the *FLP* terminator, was ligated into the *Ecl*136II-opened pRS415 (ATCC 87520) and pRS425 (ATCC 77106) plasmids, obtaining the low-copy centromeric pRS415Bax and the high-copy episomal pRS425Bax expression plasmids.

Results

Single colonies of yeast cells transformed with pRS415 or pRS415Bax or pRS425 or pRS425Bax were grown in 10 ml minimal glucose-containing medium with vigorous aeration at 30°C to an optical density of 1 OD_{600}. Cells were pelleted by centrifugation and washed two times with sterile dH_2O before resuspending in 10 ml minimal galactose-containing medium. After culturing for various times at 30°C, the total cell density of the cultures was determined, and 1000 cells were spread on minimal glucose-based semisolid medium, followed by incubation at 30°C for 3 days. The number of colonies on plates from the 0 hr cultures was designated as 100% (Fig. 4).

Example 8. Bax Expression in Candida cells

Strains

The *Candida albicans* strain CAI4 (*ura3*≅) was used to perform the experiments (Fonzi and Irwin 1993).

E. coli transformations were done using the Top10 strain from Invitrogen (San Diego, CA, USA) (F' *mcr*A ≅(*mrr-hsd*RMS-*mcr*BC) ≅80*lac*Z□M15 ≅*lac*X74 *deo*R *rec*A1 *ara*D139 ≅(*ara-leu*)7697 *gal*U *gal*K *rps*L (Str^R) *end*A1 *nup*G).

Media

Synthetic dextrose media (SD), containing 2% glucose, 1.34% Yeast Nitrogen Base without amino acids and 0.77g/l CSM-ura (Bio 101, Vista, CA, USA) was used to grow the *Candida albicans* transformants. In case of the wild type (CAI4), the media was supplemented with

50µg/ml uridine. To prepare plates the media was solidified with 2% agar. Expression of the synthetic *BAX* gene was performed using 2% galactose as carbon source.

Construction of the codon-optimised *BAX* gene

Construction of the synthetic BAX gene followed the nomenclature described for *Candida albicans* (Lloyd and Sharp 1992; Brown, *et al.* 1991; http://alces.med.umn.edu/candida/codons.html; http://www.kazusa.or.jp/codon). To ensure a high expression of the synthetic gene, the subset of 'optimal' codons of highly expressed genes was used to design the synthetic *BAX* gene.

The synthCa*BAX* gene was constructed in three parts using eight oligonucleotides (Fig. 5). The sequences of the oligonucleotides are given in Table 7. Primer A1 introduced upstream of the ATG codon a *Pst* I site and a *Bgl* II site. The *Pst* I site was used later on for direct cloning into the *Candida albicans* expression vector, while the *Bgl* II site served as a linker for a y*EGFP* fusion. Primer C2 introduced a *Sma* I site, suitable for cloning into the expression vector.

Fragment A and B were synthesised in two steps: in a first PCR round primer X1 and X2 (X represents A or B, respectively) were used together. The resulting fragment served as a template in a second PCR round together with primers X1 and X3. Fragment C was synthesised in a single PCR round using the primers C1 and C2. Fragment A and B were cloned into the pCR-BluntII-TOPO vector (Stratagene), while fragment C was cloned into the pCR2.1-TOPO vector (Stratagene). All three fragments were sequenced to ensure that no mutation was introduced by the PCR.

Subsequently, fragment A was digested with *Pst* I and *Taq* I, fragment B wit *Taq* I and *Bam HI* and fragment C with *Bam* HI and *Sma* I. The three products were cloned in a quadruple ligation into pUC21 digested with *Pst* I and *Sma* I resulting in the plasmid pUC21:synthCandidaBAX. The sequence of the synthetic BAX gene is shown in Figure 6.

Construction of synthetic *BAX*- and *GFP*-synthetic *BAX* expression plasmids

A *Pst* I-*Sma* I fragment containing the ORF of the synthetic BAX gene was cloned into the *Pst* I-*Stu* I digested vector pGAL1ACT1LUC (W. Martinet, EP application nr 99204557.5) resulting in the expression construct pGAL1P:synthCa*BAX* (Fig. 7A). To facilitate recognition of the AUG codon during formation of initiation complexes a purine base (A) was introduced at position –3 from the AUG codon (Kozak 1981) using the Quick change site directed mutagenesis kit from Stratagene.

The yeast enhanced *GFP* gene y*EGFP*, (Cormack *et al.* 1997) was amplified by PCR using primer 5'-AA***CTGCAGA*****TG**TCTAAAGGTGAAGAATTATTC-3' (SEQ ID NO 11) as upstream primer and primer 5'-GGA***AGATCT***TCCTTTGTACAATTCATCC ATACC-3' (SEQ ID NO 12) as

downstream primer. The sense primer introduced a *Pst* I site (shown in bold and italic), while the anti-sense primer contained a *Bgl* II linker (shown in bold and italic) for fusion with the synthetic *BAX* gene. After cloning of the yEGFP gene into the pCR2.1-TOPO vector (Stratagene), the gene was sequenced to ensure that no mutation was introduced by PCR.

The y*EGFP*-synth Candida *BAX* fusion was created by cloning a *Pst*I-*Bgl*II y*EGFP* fragment together with a *Bgl* II-*Sma* I synthetic Candida *BAX* fragment into the *Pst* I-*Stu* I digested expression vector pGAL1ACT1LUC. The obtained pGAL1P:y*EGFP*-synthCa*BAX* fusion construct (Fig.7B) was sequenced to ensure that no frameshift had occurred.

Creation of the synthetic *BAX* expression strains

Transformation of the expression plasmids was performed using a modified procedure (Logghe, unpublished) of the spheroblasting protocol (Herreros *et al.* 1992). The plasmids were linearised with *Bpu*1102 I to allow directed integration into the genome at the GAL1 promoter site. Correct integration was analysed by Southern blotting. Therefore genomic DNA from different transformants was prepared using the Nucleon® extraction and purification kit (Amersham Pharmacia Biotech) and digested with *Xba* I. The BAX probe used in the Southern blot was prepared by PCR. The PCR was performed using the pGAL1P:synthCa*BAX* plasmid as template, together with the sense primer 5'-ATGGATGGTTCTGGTGAAC-3' (SEQ ID NO 13) and the anti-sense primer 5'-TTAACCCATTTTTTTCCAGATG-3' (SEQ ID NO 14). Standard PCR conditions were used. For detection of the y*EGFP* a probe was synthesised by PCR using primer 5'-AGAGATCTCGAGGGATCC-3' (SEQ ID NO 15) as sense primer and primer 5'-GCATTATTTGTACAATTCATCC-3' (SEQ ID NO 16) as anti-sense primer. Southern blot hybridisation and detection were performed using the AlkPhos DIRECT labelling and detection system (Amersham Pharmacia Biotech) following the instructions of the manufacturer.

Western blot analysis

For Western blot analysis cells were pre-grown over night in SD-ura media till late log phase. The cells were harvested by centrifugation, washed twice with water and inoculated in SG-ura to induce Bax expression. Induction was performed for 15 hours. Yeast crude extracts were prepared as described before (Sambook, Fritsch *et al.* 1989). Detection of the Bax protein was performed using a polyclonal rabbit anti-mouse /rat Bax antibody (Pharmingen). Due to contamination of this antibody with yeast cell wall mannan antibodies, a very high background occurred. This problem could be avoided by pre-incubation of the antibody with 0.5mg/ml purified yeast mannan (Rossanese *et al.* 1999). Detection of the Gfp protein was done using an anti-Gfp monoclonal antibody (Molecular Probes, Eugene, OR, USA).

Growth curves

For growth curves, yeast cells were grown for 24 h in SD-ura medium (supplemented with uridine for the wild type). These cultures were harvested, washed twice with water and inoculated to an OD_{600} of 0.1 into fresh SD-ura or SG-ura media. Growth was monitored in microtitre plates using the Bioscreen C system (Labsystems).

Viability tests

Cells were pregrown in minimal dextrose medium to an OD_{600} of 1. After washing the cells twice with water they were switched to minimal medium containing galactose as carbon source. At the time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represent the viable fraction of the pool.

Results : Conditional expression of the synthetic *BAX* gene in *Candida albicans*

A cDNA encoding the full-length mouse Bax protein was placed under control of the *Candida albicans* GAL1 promoter allowing for conditional expression when cells are grown in galactose containing media. Initial experiments were performed using the wild type mouse *bax* gene. Expression of this gene did not result in any detectable phenotype, no difference in growth compared to the wild type was observed when cells were grown on galactose containing media (data not shown). This could be due to the non-traditional codon strategy adopted by *Candida albicans* and related species. Analysis of the codons used in the mouse *BAX* gene revealed a for *Candida albicans* not optimal codon usage as found for highly expressed genes in this yeast. To ensure a high expression of the *BAX* gene a codon-adapted, synthetic version of the gene was created using the strategy described above. The synthetic *BAX* gene was fused to the yE*GFP* to allow screening for transformants with a high yE*GFP*-synthCa*BAX* expression level using FACS technology. The newly obtained plasmids pGAL1P:synthCa*BAX* and pGAL1:*GFP*-synthCa*BAX* were transformed into the *C. albicans* CAI4 strain. Transformants were selected on uridine-fee minimal medium. About 25 transformants of each expression construct were chosen and streaked onto minimal dextrose medium (non-inducing conditions) as well as on minimal galactose medium (inducing conditions). After two days incubation at 30ºC all transformants did grow on the glucose containing media. When galactose was used as a sole carbon source, most of the transformants did not grow (Fig. 8). Southern blot analysis of the galactose negative transformants revealed that a copy of the synthCa*BAX* gene had been integrated into the endogenous copy of the GAL1 promoter. To study differences in growth, the transformants were grown over night in synthetic glucose containing medium. Subsequently, cells were washed with water and switched to fresh medium containing galactose as carbon source. While the wild type strain did grow well on galactose containing media no growth was

observed for the Bax expressing transformants (Fig. 9A and B). Western blot analysis of the synthCa*BAX* transformants showed accumulation of the Bax protein (15 hours Bax induction, Fig. 10). A similar result was observed when immunoblotting was performed with the *GFP*-synthCa*BAX* expressing strains. Here the fusion protein was detected at the expected molecular weight of about 45K under inducing conditions (galactose as carbon source). In addition to the fusion protein a band appeared at the molecular weight of about 20K. This corresponds to the molecular weight of the Gfp protein alone. Addition of a Gfp-expressing strain as a positive control to the western blot did confirm these results. Here the Gfp protein was detected at the same molecular weight as the unexpected band in the *GFP*-synthCa*BAX* expressing strain (Fig. 11). This is most probably due to a partly proteolytic degradation of the fusion protein. Analysis of the Gfp-fluorescence using FACS technology showed a high Gfp-fluorescence signal for the transformants expressing the fusion protein (Fig. 12). When cell viability was analysed, different results were obtained for the synthCa*BAX* strain and the *GFP*-synthCa*BAX* strain. The synthCa*BAX* strain showed quite a rapid decrease in the amount of colony forming units during the first 6 hours of incubation on galactose containing media. Afterwards the process slowed down significantly. This is in contrast to the results obtained for the strain expressing the gfp-synthCabax fusion protein. Here almost all the cells died at a very rapid rate during the first 3 hours of incubation in media containing galactose as sole carbon source. It is possible that the Bax trigger in the synthCabax expressing cells is not strong enough to kill all cells. The cell has enough time to activate a sort of defence mechanism, possibly by proteolytic degradation of the Bax protein. The situation is different for the fusion protein. Gfp is a very stable protein itself. Fusion of the Gfp to another protein could result in a stabilisation of this protein. It would be more resistant to proteolytic degradation. This would explain the situation for the Gfp-Bax fusion. The Gfp-Bax protein is more protected from proteolytic degradation. Like that it is for a longer period present in the cell. The death trigger is herewith stronger, so the cells die faster. The time that the cells have to activate the proteolytic machinery is not sufficient for them to survive.

Table 1:

Oligo	Sequence 5' → 3'
	AA*CTGCAGGAAGATCTTCCATG*GATGGTTCTGGTGAACAATTGGGTTCTGGTGG
A1	TCCAACCTCTTCTGAACAAATCATGAAAACCGGTGCTTTCTTGTTG (SED ID NO 3)
	TAGAAGCATCTTGTGGTGGTTGTTCCAAGGTCAATTCTGGGGTTTCACCAGCC
A2	ATTCTACCAGCTCTATCTTGGATGAAACCTTGCAACAAGAAAGCACC (SEQ ID NO 4)
	GGAATTC*TCGAC*ATCAGCGATCATTCTTTGCAATTCCATGTTAGAATCCAATTC
A3	ATCACCGATTCTTCTCAAACATTCAGACAATTTTTTGGTAGAAGCATCTTGTG (SEQ ID NO 5)
B1	GGAATTCGCTGATG*TCGAT*ACCGATTCTCCAAGAAGTCTTCTTCAGAGTCG
	CTGCTGATATGTTCGCTGATGGTAACTTCAACTG (SED ID NO 6)
B2	AATTCTGGGACTTTGGTACACAAAGCTTTCAAGACCAATTTAGAAGCGAAGTA
	GAACAAAGCGACGACTCTACCCCAGTTGAAGTTACCA (SEQ ID NO 7)
B3	CCACCTTGATCTT*GGATCC*AGACCAACAATCTTTCTCTCAAGAAATCCAAGGTC
	CAACCCATGATGGTTCTGATCAATTCTGGGACTTTG (SEQ ID NO 8)
C1	ATTGTTGGTCT*GGATCC*AAGATCAAGGTGGTTGGGAAGGTTTGTTGTCTTACTT
	CGGTACCCCCAACCTGGCAAACCGTCA (SEQ ID NO 9)
C2	TCC*CCCGGGGGA*TTAACCCATTTTTTTCCAGATGGTCAAAGAAGCGGTCAAGAC
	ACCAGCGACGAAGATGGTGACGGTTGCCAGGTTGGG (SEQ ID NO 10)

Table 2: Overview of the differentially expressed genes after 30 min Bax expression

Comparison: INVSc1 YIpUTL versus INVSc1 YIpUTyLB

ORF	Gene	Normalised Intensities YLB		Up/down	Ch value
Cellular role : Cell cycle control					
YBR133C	*HSL7*	18932.54	37877.20	↑	2.00
Cellular role : Polymerase II transcription					
YDR253C	*MET32*	17661.13	45567.17	↑	2.58
YBR112C	*SSN6*	26698.87	65315.83	↑	2.45
YDR145W	*TAF61*	38697.96	73117.62	↑	1.89
YBR289W	*SNF5*	33111.77	72328.70	↑	2.18
YDR216W	*ADR1*	30127.45	8815.87	↓	3.42
YEL009C	*GCN4*	16533.76	3030.44	↓	5.46
YBR089C-A	*NHP6B*	22698.63	6297.49	↓	3.60
YMR043W	*MCM1*	39141.64	84180.45	↑	2.15
YKR092C	*SRP40*	5965.63	16105.82	↑	2.70
YMR273C	*ZDS1*	14699.61	35508.04	↑	2.42
YPL089C	*RLM1*	34922.91	67856.88	↑	1.94
YOR372C	*NDD1*	20285.12	44445.20	↑	2.19
YPL037C	*EGD1*	30633.33	5250.70	↓	5.83
Cellular role : Cell polarity					
YBL085W	*BOI1*	7693.29	18614.99	↑	2.42
Cellular role : Chromatine structure					
YBR009C	*HHF1*	16668.00	4178.80	↓	3.99
YNL030W	*HHF2*	49878.04	12566.96	↓	3.97
YDR224C	*HTB1*	67355.40	23156.82	↓	2.91
YBL002W	*HTB2*	25269.02	5383.97	↓	4.69
Cellular role: RNA processing					
YER112W	*USS1*	12776.74	31470.70	↑	2.46
YPL190C	*NAB3*	6381.36	17892.11	↑	2.80
YNL112W	*DBP2*	9956.84	28036.48	↑	2.82
Cellular role: Energy generation					
YPL078C	*ATP4*	26902.69	5980.38	↓	4.50
YDL004W	*ATP16*	36525.08	3004.34	↓	12.16
YDR377W	*ATP17*	14419.41	756.86	↓	19.05
YDR529C	*QCR7*	35346.95	5394.65	↓	6.55
YGR008C	*STF2*	13275.51	2276.27	↓	5.83
YEL039C	*CYC7*	13604.38	2689.66	↓	5.06
YKL150W	*MCR1*	105337.67	30743.75	↓	3.43
YLR038C	*COX12*	52687.73	5455.83	↓	9.66
YLR327C		113.966.77	54,014.65	↓	2.11
Cellular role: Carbohydrate metabolism					
YBR149W	*ARA1*	15149.55	4095.17	↓	3.70
YHR094C	*HXT1*	12526.90	785.73	↓	15.94
YDR345C	*HXT3*	36643.13	1632.48	↓	22.45
YDR343C	*HXT6*	77064.71	32060.05	↓	2.40
YDR342C	*HXT7*	76349.13	27615.15	↓	2.76
Cellular role: Signal transduction					
YER177W	*BMH1*	22856.29	44771.71	↑	1.96
YDR099W	*BMH2*	40127.38	74572.38	↑	1.86

YGR070W	*ROM1*	12055.28	28169.57	↑	2.34
YGR023W	*MTL1*	7354.78	19648.06	↑	2.67
Cellular role: Protein synthesis					
YGR034W	*RPL26B*	71942.48	74625.22	↑	1.04
Cellular role: Protein folding					
YLR216C	*CPR6*	9616.80	31126.02	↑	3.24
Cellular role: Protein modification/degradation					
YFR052W	*RPN12*	5583.57	14855.67	↑	2.66
YDL147W	*RPN5*	31932.20	52939.11	↑	1.66
YGR132C	*PHB1*	15429.56	5591.19	↓	2.76
YGR135W	*PRE9*	39921.63	5517.17	↓	7.24
YFR010W	*UBP6*	1892.76	828.94	↓	2.28
Cellular role: Cell stress					
YIR037W	*GPX3*	7869.22	21789.00	↑	2.77
YDR513W	*TTR1*	55986.32	33263.12	↓	1.68
YCL035C	*GRX1*	70248.30	10969.97	↓	6.40
YFL014W	*HSP12*	41689.29	18658.48	↓	2.23
YHR053C	*CUP1A*	72852.07	43488.52	↓	1.68
YHR055C	*CUP1B*	71934.03	56799.80	↓	2.77
YMR173W	*DDR48*	16670.70	5022.40	↓	3.32
YMR251W-A	*HOR7*	26879.95	417.36	↓	64.41
YLR043C	*TRX1*	58251.39	4435.79	↓	13.13
YBL064C	*PRX1*	21525.00	40969.00	↑	1.90
YOL151W	*GRE2*	2624.55	24152.03	↑	9.20
Cellular role: Unknown					
YBL081W		73834.11	74612.35	↑	1.01
YDR366C		39998.46	57428.80	↑	1.44
YCR004C	*YCP4*	6869.06	28115.73	↑	4.09
YCR013C		3988.55	15144.34	↑	3.80
YBR050C	*REG2*	4687.91	14408.20	↑	3.07
YBL109W		18744.60	35440.24	↑	1.89
YDR154C		19565.23	69428.03	↑	3.55
YEL071W	*DLD3*	22235.73	68790.83	↑	3.09
YHR095W		14426.76	34896.68	↑	2.42
YGR069W		43413.57	72420.39	↑	1.67
YDR544C		13567.00	27004.37	↑	1.99
YGR236C		24927.59	8032.35	↓	3.10
YIL057C		24246.39	773.56	↓	31.34
YGL080W		23425.00	3217.81	↓	7.28
YGL072C		16437.52	2652.80	↓	6.20
YHR056C	*RSC30*	72072.88	57446.85	↓	1.25
YKL054C	*VID31*	17990.49	38258.80	↑	2.13
YLR311C		7992.40	24164.87	↑	3.02
YJR115W		64690.69	102066.34	↑	1.58
YJL188C	*BUD19*	7580.28	22325.70	↑	2.95
YKR040C		50934.78	100733.41	↑	1.98
YLR053C		8117.66	20317.34	↑	2.50
YOR121C		59950.94	92470.43	↑	1.54
YNL143C		98911.28	110534.34	↑	1.12
YOR131C		7941.55	22353.72	↑	2.81
YNL338W		21800.45	38777.28	↑	1.78
YNL179C		13729.36	39516.53	↑	2.88
YOL150C		3408.74	60298.39	↑	17.69

YMR107W		65118.70	10042.46	↓	6.48
YKL065C	YET1	69556.19	12804.88	↓	5.43
YJR096W		21780.37	10655.13	↓	2.04
YJL161W		16468.73	2618.26	↓	6.29
YML128C	MSC1	80130.20	13795.84	↓	5.81
YMR251W		26879.95	417.36	↓	64.41
YMR173W-A		110104.98	61951.23	↓	1.78
YPL201C		17913.32	5018.97	↓	3.57
YOR285W		64074.73	29749.43	↓	2.15
YOR286W		13458.08	733.06	↓	18.36
Cellular role: Cell wall maintenance					
YKR076W	ECM4	2674.15	13040.04	↑	4.88
YLR390W	ECM19	5472.05	15145.85	↑	2.77
Cellular role: Membrane fusion					
YHR138C		19921.35	3707.57	↓	5.37
Cellular role : Vesicular transport					
YHR161C	YAP180A	13086.35	30160.90	↑	2.30
YPL085W	SEC16	6668.57	15206.49	↑	2.28
YKL196C	YKT6	18933.84	2890.07	↓	6.55
YPR028W	YIP2	25434.34	2049.47	↓	12.41
Cellular role : DNA repair/recombination					
YDL059C	RAD59	1948.61	13089.13	↑	6.72
Cellular role : DNA synthesis					
YEL032W	MCM3	23422.85	44327.48	↑	1.89
Cellular role : Amino acid metabolism					
YIL074C	SER33	3978.42	16702.66	↑	4.20
YGR155W	CYS4	4184.59	19270.89	↑	4.61
Cellular role : Fatty acid metabolism					
YHR179W	OYE2	2291.36	40274.02	↑	17.58
Cellular role : Protein translocation					
YNL131W	TOM22	16287.21	1679.78	↓	9.70
Cellular role : Small molecule transport					
YDR276C	SNA1	21148.46	1580.68	↓	13.38
YOR267C	HRK1	62689.30	110516.24	↑	1.76
YHR039-C	VMA10	60107.90	8490.93	↓	7.08
YOR382W	FIT2	6780.82	27236.15	↑	4.02

Table 3: Overview of the differentially expressed genes after 1h Bax expression

Comparison: INVSc1 YIpUTL versus INVSc1 YIpUTyLB

ORF	Gene	Normalized Intensities		Up/Down	Q-value
		UL	MB		
Cellular role : Polymerase II transcription					
YDR145W	*TAF61*	20729.58	57376.27	↑	2.77
YDR216W	*ADR1*	5925.91	18459.00	↑	3.11
YBR112C	*CYC8*	50186.77	64511.50	↑	1.29
YMR043W	*MCM1*	21011.54	53700.49	↑	2.56
YPL089C	*RLM1*	23440.54	64284.32	↑	2.74
YOR372C	*NDD1*	26412.58	50804.99	↑	1.92
Cellular role : Cell cycle control					
YBR133C	*HSL7*	18761.64	53238.86	↑	2.84
Cellular role : Cell polarity					
YBL085W	*BOI1*	37895.40	57761.52	↑	1.52
Cellular role : Chromatine structure					
YDR224C	*HTB1*	13661.40	55656.34	↑	4.07
Cellular role: Energy generation					
YGR183C	*QCR9*	23181.54	81865.40	↑	3.53
YLR294C		5054.57	28994.72	↑	5.74
YKL150W	*MCR1*	43663.07	60593.16	↑	1.39
YMR256C	*COX7*	7606.58	28801.54	↑	3.79
YOL126C	*MDH2*	34144.61	65326.97	↑	1.91
YLR327C		97415.94	101651.17	↑	1.04
Cellular role: Vesicular transport					
YHR161C	YAP180A	11602.81	34695.20	↑	2.99
YLR206W	*ENT2*	14439.24	34621.70	↑	2.40
Cellular role: Carbohydrate metabolism					
YDR342C	*HXT7*	65273.56	22231.06	↓	2.94
YDR343C	*HXT6*	43572.28	6075.38	↓	7.17
YDR345C	*HXT3*	76352.52	40296.00	↓	1.89
YGR192C	*TDH3*	38472.30	14145.84	↓	2.72
YKR097W	*PCK1*	22919.81	38225.98	↑	1.67
YOR374W	*ALD4*	33711.37	2607.43	↓	12.93
Cellular role: Signal transduction					
YER177W	*BMH1*	16298.14	31748.91	↑	1.95
YDR099W	*BMH2*	50572.45	65123.58	↑	1.29
Cellular role: Cell wall maintenance					
YLR110C	*CCW12*	102525.29	11230.41	↓	9.13
Cellular role: Protein modification/degradation					
YOR261C	*RPN8*	12575.49	32568.47	↑	2.59
Cellular role: Cell stress					
YHR053C	*CUP1A*	32531.53	63579.94	↑	1.95
YHR055C	*CUP1B*	27939.92	65142.82	↑	2.33
YMR173W	*DDR48*	38338.83	60514.70	↑	1.58
YOR031W	*CRS5*	2922.32	23848.60	↑	8.16

YLR109W	*AHP1*	43067.08	6302.46	↓	6.83
Cellular role: Unknown					
YBL081W		82476.13	44279.86	↑	1.86
YBL109W		22996.63	63428.23	↑	2.76
YDR366C		14599.17	46494.73	↑	3.18
YDR154C		21296.57	56534.93	↑	2.65
YGR236C	*SPG1*	17717.80	64439.96	↑	3.64
YHR056C	*RSC30*	27020.16	65110.42	↑	2.41
YGR182C		8171.02	34669.96	↑	4.24
YDR544C		14797.70	37704.91	↑	2.55
YHR162W		13836.79	33381.64	↑	2.41
YGR243W		30829.66	59765.39	↑	1.94
YBR050C	*REG2*	14008.24	29603.16	↑	2.11
YEL071W	*DLD3*	19487.41	35273.39	↑	1.81
YDR133C		83074.54	62986.96	↓	1.32
YDR134C		83111.03	16839.53	↓	4.94
YHL021C		46028.06	8577.00	↓	5.37
YKL054C	*VID31*	28018.46	66537.91	↑	2.37
YLR311C		7803.52	31160.73	↑	3.99
YMR107W		13453.15	78850.98	↑	5.86
YKL066W		8751.84	24129.32	↑	2.76
YMR173W-A		38338.83	60514.70	↑	1.58
YML053C		23670.86	66254.48	↑	2.80
YOR121C		17039.58	58016.58	↑	3.40
YOL106W		19917.67	69853.66	↑	3.51
YNL338W		17864.90	49911.08	↑	2.79
YJR115W		84858.02	98161.71	↑	1.16
Cellular role: Small molecule transport					
YOR267C	*HRK1*	90123,84	96824,51	↑	1,07

Table 4: Overview of the differentially expressed genes after 2h Bax expression

Comparison: INVSc1 YIpUTL versus INVSc1 YIpUTyLB

ORF	Gene	Normalised Intensities		Up/Down	Fold value
		L	YLB		
Cellular role: Protein modification/degradation					
YCL052C	*PBN1*	5264.22	8175.70	↑	1.55
YDL147W	*RPN5*	22386.40	47857.67	↑	2.14
YOR261C	*RPN8*	27349.25	42198.05	↑	1.54
YGR132C	*PHB1*	5252.03	8459.53	↑	1.61
YBR139W		9458.26	3611.21	↓	2.62
Cellular role : Unknown					
YDR202C	*RAV2*	7483.71	10089.19	↑	1.35
YBR062C		4893.97	9894.82	↑	2.02
YDR366C		25468.2	59682.92	↑	2.34
YBL109W		24803.62	37444.64	↑	1.51
YDR154C		21166.26	33434.35	↑	1.58
YEL071W	*DLD3*	34153.85	44083.39	↑	1.29
YGR236C	*SPG1*	18978.52	31419.12	↑	1.85
YGR182C		30569.31	58805.05	↑	1.92
YDR544C		15937.14	24421.99	↑	1.53
YHR162W		26610.34	33794.73	↑	1.27
YHR056C	*RSC30*	33372.66	68425.24	↑	2.05
YDR133C		75520.99	62984.59	↓	1.20
YCR010C	*ADY2*	17240.59	11835.82	↓	1.46
YDR134C		72723.66	9776.23	↓	7.44
YGR069W		65418.73	53767.35	↓	1.22
YIL057C		16510.16	2198.04	↓	7.51
YGL072C		12209.68	6509.91	↓	1.88
YGL080W		22550.76	11525.24	↓	1.96
YLR311C		11095.31	24660.47	↑	2.22
YJR115W		74757.79	103422.48	↑	1.38
YMR099C		7057.15	11477.42	↑	1.63
YMR173W-A		31901.05	48886.91	↑	1.47
YML132W	*COS3*	24648.97	34895.33	↑	1.42
YKL066W		13581.94	25433.97	↑	1.87
YJL142C		7205.86	11920.21	↑	1.65
YLR346C		6447.57	11569.63	↑	1.79
YLR053C		41161.10	78636.82	↑	1.91
YMR110C		19410.64	29661.23	↑	1.53
YKR075C		19104.57	29948.72	↑	1.57
YOR121C		36492.56	59452.09	↑	1.63

Cellular role : Unknown					
YOL106W		31382.10	76664.72	↑	2.44
YNL338W		24117.93	38981.22	↑	1.62
YNL134C		9617.33	14613.60	↑	1.52
YKL065C	YET1	52422.65	33794.03	↓	1.55
YMR009W		20666.22	9519.29	↓	2.17
YJL144W		10316.92	3122.77	↓	3.30
YML126C	MSC1	584128.13	25434.11	↓	2.29
YNL179C		21938.96	10883.98	↓	2.02
YOL109W	ZEO1	22711.98	6581.11	↓	3.45
YNR002C	FUN34	18241.25	9752.25	↓	1.87
Cellular role: Chromatine structure					
YDR224C	HTB1	25356.73	30827.54	↑	1.22
YBL002W	HTB2	9241.68	14261.54	↑	1.54
YBL003C	HTA2	3453.55	6553.49	↑	1.90
YNL031C	HHT2	13376.02	2348.84	↓	5.69
Cellular role: Polymerase II transcription					
YBR289W	SNF5	59542.27	65885.13	↑	1.11
YDR073W	SNF11	12190.01	23088.03	↑	1.89
YMR043W	MCM1	66457.16	77022.05	↑	1.16
YPL089C	RLM1	49844.99	60624.28	↑	1.22
Cellular role : Signal transduction					
YDR099W	BMH2	55902.13	73874.51	↑	1.32
Cellular role: Cell stress					
YBL064C	PRX1	11203.87	14815.42	↑	1.32
YBR101C		25016.27	35781.64	↑	1.43
YLR043C	TRX1	10864.53	3912.03	↓	2.78
YGR209C	TRX2	30492.33	37829.20	↑	1.24
YER103W	SSA4	8763.38	15799.18	↑	1.80
YHR055C	CUP1B	18824.43	77613.05	↑	4.12
YHR053C	CUP1A	32726.62	63536.72	↑	1.94
YDR256C	CTA1	9614.29	4232.17	↓	2.27
YCR021C	HSP30	8090.05	3604.78	↓	2.24
YCL035C	GRX1	28437.57	12843.99	↓	2.21
YGR086C		36796.12	24272.57	↓	1.52
YFL014W	HSP12	61868.64	23288.19	↓	2.66
YOR031W	CRS5	6015.69	14519.12	↑	2.41
YMR251W-A	HOR7	17731.14	4231.39	↓	4.19
YOR120W	GCY1	114252.98	78052.05	↓	1.46
Cellular role: Protein synthesis					
YAL003W	EFB1	3044.80	5772.68	↑	1.90
YOL127W	RPL25	6266.96	12055.41	↑	1.92
YHR010W	RPL27	4057.16	10856.34	↑	2.68
YLR325C	RPL38	5401.85	12955.89	↑	2.40
YJL189W	RPL39	2044.64	8010.67	↑	3.92
YIL148W	RPL40A	5052.35	11595.54	↑	2.30
YKR094C	RPL40B	3994.57	10011.13	↑	2.54
YOL139C	CDC33	4132.18	8956.14	↑	2.17

Cellular role : Protein folding					
YLR216C	*CPR6*	20353.43	32713.37	↑	1.61
YKL117W	*SBA1*	11144.25	1500.56	↓	7.43
Cellular role: Vesicular transport					
YCR009C	*RVS161*	5350.32	9780.92	↑	1.83
YHR161C	*YAP180A*	25136.63	32461.67	↑	1.29
YBL078C	*AUT7*	16528.91	9843.25	↓	1.68
Cellular role : Carbohydrate metabolism					
YBL058W	*SHP1*	4626.50	8179.94	↑	1.77
YBR149W	*ARA1*	30706.41	9637.76	↓	3.19
YDR178W	*SDH4*	14880.91	6237.35	↓	2.39
YHR094C	*HXT1*	30389.99	18383.00	↓	1.65
YMR011W	*HXT2*	39524.90	21221.96	↓	1.86
YDR345C	*HXT3*	77025.40	56749.40	↓	1.36
YDR343C	*HXT6*	73149.70	8676.17	↓	8.43
YDR342C	*HXT7*	75331.76	27052.43	↓	2.78
YKL060C	*FBA1*	16273.54	21323.23	↑	1.31
Cellular role : Cell cycle control					
YBR133C	*HSL7*	32903	41964.32	↑	1.28
Cellular role : Energy generation					
YMR256C	*COX7*	18558.01	40422.91	↑	2.18
YML129C	*COX14*	11418.54	21798.88	↑	1.91
YFR033C	*QCR6*	9159.48	13398.67	↑	1.46
YDR529C	*QCR7*	24821.75	16556.87	↓	1.50
YJL166W	*QCR8*	15554.30	24509.26	↑	1.58
YHR001W-A	*QCR10*	12416.35	23465.31	↑	1.89
YBR039W	*ATP3*	11709.79	3088.19	↓	3.79
YPL078C	*ATP4*	11325.64	13769.72	↑	1.22
YPL271W	*ATP15*	3261.75	7839.05	↑	2.40
YLR327C		51742.90	128511.27	↑	2.48
YLR294C		15832.61	38544.44	↑	2.43
YAL060W	*FUN49*	11792.72	5778.91	↓	2.04
Cellular role: Small molecule transport					
YDR276C	*SNA1*	19337.39	12392.29	↓	1.56
YGR197C	*SNG1*	4766.18	10484.09	↑	2.20
YHR039C-B	*VMA10*	21190.93	10592.98	↓	2.00
YOR267C	*HRK1*	111849.17	101339.10	↓	1.10
Cellular role: RNA processing					
YGR250C		8709.92	17358.43	↑	1.99
Cellular role : Cell wall maintenance					
YER150W	*SPI1*	55592.73	22403.59	↓	2.48
YLR110C	*CCW12*	35147.41	5786.88	↓	6.07
Cellular role : Cell polarity					
YOR122C	*PFY1*	14459.45	20176.41	↑	1.40
Cellular role : Amino acid metabolism					
YPR035W	*GLN1*	20894.14	7522.05	↓	2.78

Table 5: Overview of the differentially expressed genes after 3h Bax expression

Comparison: INVSc1 YIpUTL versus INVSc1 YIpUTyLB

ORF	Gene	Normalized Intensities		Up/Down	Ratio
		YIpUTL	YIpUTyLB		
Cellular role : Cell cycle control					
YBR133C	*HSL7*	63562.10	43191.28	↓	1.47
Cellular role : Cell polarity					
YBL085W	*BOI1*	32734.79	23497.41	↓	1.39
Cellular role : Chromatine structure					
YDR545W	*YRF1-1*	20111.51	11479.67	↓	1.75
Cellular role: Energy generation					
YCR005C	*CIT2*	11882.42	25632.94	↑	2.16
YGR183C	*QCR9*	74474.20	11510.99	↓	6.47
YOL126C	*MDH2*	55984.88	17978.10	↓	3.11
Cellular role: Carbohydrate metabolism					
YBR019C	*GAL10*	3092.50	15697.54	↑	5.08
YDR345C	*HXT3*	14086.41	25657.66	↑	1.82
YKR097W	*PCK1*	50736.44	20858.02	↓	2.43
Cellular role: Signal transduction					
YDR099W	*BMH2*	63285.16	56028.91	↓	1.13
Cellular role: Protein synthesis					
YHR010W	*RPL27A*	23254.90	7217.14	↓	3.22
YLR325C	*RPL38*	26725.96	9121.29	↓	2.93
Cellular role: Cell stress					
YFL014W	*HSP12*	40848.44	69781.91	↑	1.71
YHR053C	*CUP1A*	20399.10	65037.14	↑	3.19
YHR055C	*CUP1B*	21763.09	64594.58	↑	2.97
YMR173W	*DDR48*	75407.16	36354.37	↓	2.07
YOL052C-A	*DDR2*	20479.72	33702.23	↑	1.65
Cellular role: Unknown					
YIL057C		7602.78	24104.02	↑	3.17
YHR056C	*RSC30*	41473.41	64809.08	↑	1.56
YDR544C		55075.67	29731.72	↓	1.85
YKR040C		48049.71	59649.47	↑	1.24
YNL338W		86107.91	30045.62	↓	2.87
YJR115W		74889.58	81238.98	↓	1.08
YBL109W		64754.79	57185.99	↓	1.13
YMR173W-A		75407.16	36354?37	↓	2.07

Table 6: Overview of the differentially expressed genes after 6h Bax expression

Comparison: INVSc1 YIpUTL versus INVSc1 YIpUTyLB

ORF	Gene	Normalized Intensities		Up/down	Change
		YIpUTL	YIpUTyLB		
Cellular role: Cell stress					
YDR171W	*HSP42*	13484.04	27183.07	↑	2.02
YFL014W	*HSP12*	41197.12	29081.08	↓	1.42
YDR513W	*TTR1*	19985.22	12935.62	↓	1.54
YCL035C	*GRX1*	31735.39	12930.71	↓	2.45
YGR209C	*TRX2*	54455.65	47569.21	↓	1.14
YHR053C	*CUP1A*	81488.84	15289.39	↓	5.33
YHR055C	*CUP1B*	81278.95	20031.69	↓	4.06
YMR251W-A	*HOR7*	18824.54	5914.28	↓	3.18
Cellular role: Signal transduction					
YDR099W	*BMH2*	29412.99	58598.42	↑	1.99
Cellular role: Protein synthesis					
YGL147C	*RPL9A*	13655.66	1585.97	↓	8.61
YGR085C	*RPL11B*	27465.15	3791.35	↓	7.24
YDR418W	*RPL12B*	14417.77	1555.24	↓	9.27
YLR029C	*RPL15A*	37122.11	9321.81	↓	3.98
YOR312C	*RPL20B*	50334.94	5706.59	↓	8.82
YBR191W	*RPL21A*	21740.90	2571.30	↓	8.46
YPL079W	*RPL21B*	31059.43	5023.61	↓	6.18
YOL127W	*RPL25*	75971.72	11749.17	↓	6.47
YHR010W	*RPL27A*	45716.64	8096.40	↓	5.65
YDR471W	*RPL27B*	14636.79	2613.40	↓	5.60
YDL075W	*RPL31A*	11969.47	2611.53	↓	4.58
YBL092W	*RPL32*	7872.80	857.85	↓	9.18
YDL191W	*RPL35A*	28582.59	6046.25	↓	4.73
YDL136W	*RPL35B*	25433.49	5064.51	↓	5.02
YLR325C	*RPL38*	48051.23	8217.18	↓	5.85
YIL148W	*RPL40A*	47028.95	9543.65	↓	4.93
YKR094C	*RPL40B*	39900.50	5957.78	↓	6.70
YHR141C	*RPL42B*	10163.88	937.21	↓	10.84
YML063W	*RPS1B*	15916.48	1144.54	↓	13.91
YGL123W	*RPS2*	12505.56	2243.26	↓	5.57
YOR096W	*RPS7A*	24164.37	3223.60	↓	7.50
YBL072C	*RPS8A*	17198.50	3233.30	↓	5.32
YER102W	*RPS8B*	16234.83	1791.18	↓	9.06
YBR189W	*RPS9B*	10075.22	2150.89	↓	4.68
YOR293W	*RPS10A*	51787.23	12110.74	↓	4.28
YDR064W	*RPS13*	9736.57	1587.67	↓	6.13
YDR450W	*RPS18A*	37913.71	5674.60	↓	6.68
YML026C	*RPS18B*	14458.01	2027.28	↓	7.13
YKL156W	*RPS27A*	23725.18	11117.26	↓	2.13
YLR167W	*RPS31*	38648.54	2611.97	↓	14.80
YJL138C	*TIF2*	20154.61	7264.66	↓	2.77
Cellular role: Energy metabolism					
YGR183C	*QCR9*	57357.59	80447.53	↑	1.40
YDL004W	*ATP16*	25047.95	10988.85	↓	2.28
YKL150W	*MCR1*	50931.46	37076.83	↓	1.37

YLR038C	COX12	39506.06	29534.70	↓	1.34
Cellular role: Unknown					
YDR442W		14654.61	2242.42	↓	6.54
YDR134C		17025.59	10561.72	↓	1.61
YHR056C	RSC30	81350.52	31447.10	↓	2.59
YKR040C		48390.21	90125.88	↑	1.86
YLR414C		13463.40	8085.92	↓	1.67
YLR312C		25589.67	16184.57	↓	1.58
YJL188C	BUD19	22074.09	4526.39	↓	4.88
YOR285W		75099.98	61896.00	↓	1.21
YOL109W	ZEO1	66287.15	35502.43	↓	1.87
Cellular role: Chromatine structure					
YBR009C	HHF1	11173.15	5416.74	↓	2.06
YNL030W	HHF2	31366.74	20132.23	↓	1.56
Cellular role: Nucleotide metabolism					
YDR399W	HPT1	13339.03	5333.81	↓	2.50
Cellular role: Polymerase II transcription					
YEL009C	GCN4	34617.98	20798.63	↓	1.66
YPL037C	EGD1	17862.37	8229.01	↓	2.17
Cellular role: Vesicular transport					
YBL078C	AUT7	42661.70	32333.01	↓	1.32
YOR327C	SNC2	22716.56	13704.48	↓	1.66
Cellular role : Small molecule transport					
YHR039C-B	VMA10	44429.30	23826.51	↓	1.86
Cellular role : Cell wall maintenance					
YKL097W-A	CWP2	13529.93	1617.20	↓	8.37
Cellular role: Carbohydrate metabolism					
YKL060C	FBA1	33329.74	10367.82	↓	3.21

Table 7:

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 17	YAL003W	EFB1			1.90		
SEQ ID NO 19	YAL060W	FUN49			-2.00		
SEQ ID NO 21	YBL002W	HTB2	-4.69		1.54		
SEQ ID NO 23	YBL058W	SHP1			1.77		
SEQ ID NO 25	YBL064C	PRX1	1.90		1.32		
SEQ ID NO 27	YBL072C	RPS8A					-5.32
SEQ ID NO 29	YBL081W		1.01	1.86			
SEQ ID NO 31	YBL085W	BOI1	2.42	1.52		-1.39	
SEQ ID NO 33	YBL092W	RPL32			2.76		-9.18
SEQ ID NO 35	YBL109W		1.89	2.76	1.51	-1.13	
SEQ ID NO 37	YBR009C	HHF1	-3.99				-2.06
SEQ ID NO 39	YBR019C	GAL10				5.08	
SEQ ID NO 41	YBR039W	ATP3			-3.70		
SEQ ID NO 43	YBR050C	REG2	3.07	2.11			
SEQ ID NO 45	YBR062C				2.02		
SEQ ID NO 47	YBR089C-A	NHP6B	-3.60				
SEQ ID NO 49	YBR101C				1.43		
SEQ ID NO 51	YBR112C	SSN6	2.45	1.29			
SEQ ID NO 53	YBR133C	HSL7	2.00	2.84	1.28	-1.47	
SEQ ID NO 55	YBR139W				-2.60		
SEQ ID NO 57	YBR149W	ARA1	-3.70		-3.11		
SEQ ID NO 59	YBR189W	RPS9B					-4.68
SEQ ID NO 61	YBR191W	RPL21A					-8.46
SEQ ID NO 63	YBR289W	SNF5	2.18		1.11		
SEQ ID NO 65	YCL035C	GRX1	-6.40		-2.20		-2.45
SEQ ID NO 67	YCL052C	PBN1			1.55		
SEQ ID NO 69	YCR004C	YCP4	4.09				
SEQ ID NO 71	YCR005C	CIT2				2.16	
SEQ ID NO 73	YCR009C	RVS161			1.83		
SEQ ID NO 75	YCR010C				-1.40		
SEQ ID NO 77	YCR013C		3.80				
SEQ ID NO 79	YCR021C	HSP30			-2.20		
SEQ ID NO 81	YDL004W	ATP16	-12.16				-2.28
SEQ ID NO 83	YDL059C	RAD59	6.72				
SEQ ID NO 85	YDL075W	RPL31A					-4.58
SEQ ID NO 87	YDL147W	RPN5	1.66		2.14		
SEQ ID NO 89	YDR064W	RPS13					-6.13
SEQ ID NO 91	YDR073W	SNF11			1.89		
SEQ ID NO 93	YDR099W	BMH2	1.86	1.29	1.32	-1.13	1.99
SEQ ID NO 95	YDR133C			-1.32	-1.20		
SEQ ID NO 97	YDR134C			-4.94	-7.40		-1.61
SEQ ID NO 99	YDR145W	TAF61	1.89	2.77			
SEQ ID NO 101	YDR154C		3.55	2.65	1.58		
SEQ ID NO 103	YDR171W	HSP42					2.02
SEQ ID NO 105	YDR178W	SDH4			-2.30		
SEQ ID NO 107	YDR202C	RAV2			1.35		
SEQ ID NO 109	YDR216W	ADR1	-3.42	3.11			
SEQ ID NO 111	YDR224C	HTB1	-2.91	4.07	1.22		
SEQ ID NO 113	YDR253C	MET32	2.58				
SEQ ID NO 115	YDR256C	CTA1			-2.20		
SEQ ID NO 117	YDR276C	SNA1	-13.38		-1.50		

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 119	YDR342C	HXT7	-2.76	-2.94	-2.70		
SEQ ID NO 121	YDR343C	HXT6	-2.40	-7.17	-8.40		
SEQ ID NO 123	YDR345C	HXT3	-22.45	-1.89	-1.30	1.82	
SEQ ID NO 125	YDR366C		1.44	3.18	2.34		
SEQ ID NO 127	YDR377W	ATP17	-19.05				
SEQ ID NO 129	YDR399W	HPT1					-2.50
SEQ ID NO 131	YDR418W	RPL12B					-9.27
SEQ ID NO 133	YDR513W	TTR1	-1.68				-1.54
SEQ ID NO 135	YDR544C		1.99	2.55	1.53	-1.85	
SEQ ID NO 137	YDR545W	YRF1-1				-1.75	
SEQ ID NO 139	YEL009C	GCN4	-5.46				-1.66
SEQ ID NO 697	YEL032W	MCM3	1.89				
SEQ ID NO 141	YEL039C	CYC7	-5.06				
SEQ ID NO 143	YEL071W	DLD3	3.09	1.81	1.29		
SEQ ID NO 145	YER103W	SSA4			1.80		
SEQ ID NO 147	YER112W	USS1	2.46				
SEQ ID NO 149	YER150W	SPI1			-2.40		
SEQ ID NO 151	YER177W	BMH1	1.96	1.95			
SEQ ID NO 153	YFR010W	UBP6	-2.28				
SEQ ID NO 155	YFR033C	QCR6			1.46		
SEQ ID NO 157	YFR052W	RPN12	2.66				
SEQ ID NO 159	YGL072C		-6.20		-1.80		
SEQ ID NO 161	YGL080W		-7.28		-1.90		
SEQ ID NO 163	YGL123W	RPS2					-5.57
SEQ ID NO 165	YGR008C	STF2	-5.83				
SEQ ID NO 167	YGR023W	MTL1	2.67				
SEQ ID NO 169	YGR034W	RPL26B	1.04				
SEQ ID NO 171	YGR069W		1.67		-1.20		
SEQ ID NO 173	YGR070W	ROM1	2.34				
SEQ ID NO 175	YGR086C				-1.50		
SEQ ID NO 177	YGR132C	PHB1	-2.76		1.61		
SEQ ID NO 179	YGR135W	PRE9	-7.24				
SEQ ID NO 181	YGR155W	CYS4	4.61				
SEQ ID NO 183	YGR192C	TDH3		-2.72			
SEQ ID NO 185	YGR197C	SNG1			2.20		
SEQ ID NO 187	YGR209C	TRX2			1.24		-1.14
SEQ ID NO 189	YGR243W			1.94			
SEQ ID NO 191	YGR250C				1.99		
SEQ ID NO 193	YHL021C			-5.37			
SEQ ID NO 195	YHR001W-A	QCR10			1.89		
SEQ ID NO 197	YHR039C-B	VMA10	-7.08		-2.00		-1.86
SEQ ID NO 199	YHR053C	CUP1A	-1.68	1.95	1.94	3.19	-5.33
SEQ ID NO 201	YHR055C	CUP1B	-2.77	2.33	4.12	2.97	-4.06
SEQ ID NO 203	YHR056C		-1.25	2.41	2.05	1.56	-2.59
SEQ ID NO 205	YHR094C	HXT1	-15.94		-1.60		
SEQ ID NO 207	YHR095W		2.42				
SEQ ID NO 209	YHR138C		-5.37				
SEQ ID NO 211	YHR161C	YAP180A	2.30	2.99	1.29		
SEQ ID NO 213	YHR162W			2.41	1.27		
SEQ ID NO 215	YHR179W	OYE2	17.58				
SEQ ID NO 217	YIL057C		-31.34		-7.50	3.17	
SEQ ID NO 219	YIL074C	SER33	4.20				
SEQ ID NO 221	YIR037W	GPX3	2.77				

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 223	YJL138C	TIF2					-2.77
SEQ ID NO 225	YJL142C				1.65		
SEQ ID NO 227	YJL144W				-3.30		
SEQ ID NO 229	YJL161W		-6.29				
SEQ ID NO 231	YJL166W	QCR8			1.58		
SEQ ID NO 233	YJR096W		-2.04				
SEQ ID NO 235	YJR115W		1.58	1.16	1.38	-1.08	
SEQ ID NO 237	YKL054C	VID31	2.13	2.37			
SEQ ID NO 239	YKL060C	FBA1			1.31		-3.21
SEQ ID NO 241	YKL065C	YET1	-5.43		-1.55		
SEQ ID NO 243	YKL066W			2.76	1.87		
SEQ ID NO 245	YKL097W-A	CWP2					-8.37
SEQ ID NO 247	YKL117W	SBA1			-7.43		
SEQ ID NO 249	YKL150W	MCR1	-3.43	1.39			-1.37
SEQ ID NO 251	YKL156W	RPS27A					-2.13
SEQ ID NO 253	YKL196C	YKT6	-6.55				
SEQ ID NO 255	YKR040C		1.98			1.24	1.86
SEQ ID NO 257	YKR075C				1.57		
SEQ ID NO 259	YKR076W	ECM4	4.88				
SEQ ID NO 261	YKR092C	SRP40	2.70				
SEQ ID NO 263	YKR097W	PCK1		1.67		-2.43	
SEQ ID NO 265	YLR029C	RPL15A					-3.98
SEQ ID NO 267	YLR038C	COX12	-9.66				-1.34
SEQ ID NO 269	YLR043C	TRX1	-13.13		-2.78		
SEQ ID NO 271	YLR053C		2.50		1.91		
SEQ ID NO 273	YLR109W	AHP1		-6.83			
SEQ ID NO 275	YLR110C			-9.13	-6.07		
SEQ ID NO 277	YLR206W	ENT2		2.40			
SEQ ID NO 279	YLR216C	CPR6	3.24		1.61		
SEQ ID NO 281	YLR294C			5.74	2.43		
SEQ ID NO 283	YLR311C		3.02	3.99	2.22		
SEQ ID NO 285	YLR312C						-1.58
SEQ ID NO 287	YLR327C		-2.10	1.04	2.48		
SEQ ID NO 289	YLR346C				1.79		
SEQ ID NO 291	YLR390W	ECM19	2.77				
SEQ ID NO 293	YLR414C						-1.67
SEQ ID NO 295	YML053C			2.80			
SEQ ID NO 297	YML129C	COX14			1.91		
SEQ ID NO 299	YML132W	COS3			1.42		
SEQ ID NO 301	YMR009W				-2.17		
SEQ ID NO 303	YMR011W	HXT2			-1.86		
SEQ ID NO 305	YMR043W	MCM1	2.15	2.56	1.16		
SEQ ID NO 307	YMR099C				1.63		
SEQ ID NO 309	YMR107W		-6.48	5.86			
SEQ ID NO 311	YMR110C				1.53		
SEQ ID NO 313	YMR173W	DDR48	-3.32	1.58		-2.07	
SEQ ID NO 691	YMR173W-A		-1.78	1.58	1.47	-2.07	
SEQ ID NO 315	YMR251W		-64.41				
SEQ ID NO 317	YMR251W-A	HOR7	-64.41		-4.19		-3.18
SEQ ID NO 319	YMR256C	COX7		3.79	2.18		
SEQ ID NO 321	YMR273C	ZDS1	2.42				
SEQ ID NO 323	YNL030W	HHF2	-3.97				-1.56
SEQ ID NO 325	YNL031C	HHT2			-5.69		

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 327	YNL112W	DBP2	2.82				
SEQ ID NO 329	YNL131W	TOM22	-9.70				
SEQ ID NO 331	YNL134C				1.52		
SEQ ID NO 333	YNL143C		1.12				
SEQ ID NO 335	YNL179C		2.88		-2.02		
SEQ ID NO 337	YNL338W		1.78	2.79	1.62	-2.87	
SEQ ID NO 339	YNR002C	FUN34			-1.87		
SEQ ID NO 709	YOL052C-A	DDR2				1.65	
SEQ ID NO 341	YOL106W			3.51	2.44		
SEQ ID NO 343	YOL109W	ZEO1			-3.45		-1.87
SEQ ID NO 345	YOL126C	MDH2		1.91		-3.11	
SEQ ID NO 347	YOL139C	CDC33			2.17		
SEQ ID NO 349	YOL150C		17.69				
SEQ ID NO 351	YOL151W	GRE2	9.20				
SEQ ID NO 353	YOR120W	GCY1			-1.46		
SEQ ID NO 355	YOR121C		1.54	3.40	1.63		
SEQ ID NO 357	YOR122C	PFY1			1.40		
SEQ ID NO 359	YOR131C		2.81				
SEQ ID NO 361	YOR261C	RPN8		2.59	1.54		
SEQ ID NO 363	YOR267C		1.76	1.07	-1.10		
SEQ ID NO 365	YOR285W		-2.15				-1.21
SEQ ID NO 367	YOR286W		-18.36				
SEQ ID NO 369	YOR327C	SNC2					-1.66
SEQ ID NO 371	YOR372C	NDD1	2.19	1.92			
SEQ ID NO 373	YOR374W	ALD4		-12.93			
SEQ ID NO 375	YOR382W		4.02				
SEQ ID NO 377	YPL037C	EGD1	-5.83				-2.17
SEQ ID NO 379	YPL078C	ATP4	-4.50		1.22		
SEQ ID NO 381	YPL079W	RPL21B					-6.18
SEQ ID NO 383	YPL085W	SEC16	2.28				
SEQ ID NO 385	YPL089C	RLM1	1.94	2.74	1.22		
SEQ ID NO 387	YPL190C	NAB3	2.80				
SEQ ID NO 389	YPL201C		-3.57				
SEQ ID NO 391	YPL271W	ATP15			2.40		
SEQ ID NO 393	YPR028W	YIP2	-12.41				
SEQ ID NO 395	YPR035W	GLN1			-2.78		

TABLE 8

	C. albicans 522 CDS's					S. cerevisiae 11645 CDS's	
aa	codons	frequency: per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency: per thousand	total number
Ala	**GCU**	30.7	8686	x	6	21.1	118595
	GCC	12.7	3582		4	12.6	70785
	GCA	15.4	4357		2	16.2	91018
	GCG	2	578		1	6.1	34546
Arg	CGU	5.9	1682		1	6.5	36518
	CGC	0.7	204		1	2.6	14571
	CGA	3.5	989		3	3	16957
	CGG	0.8	220		3	1.7	9801
	AGA	23.6	6673	x	1	21.3	119672
	AGG	2.7	769		2	9.3	52057
Asn	**AAU**	37.9	10731	x	1	36	202351
	AAC	18.7	5293		2	24.9	140194
Asp	**GAU**	43.6	12323	x	5	37.8	212658
	GAC	14.7	4152		7	20.4	114451
Cys	**UGU**	9.7	2757	x	1	8	44797
	UGC	1.7	493		1	4.7	26357
Gln	**CAA**	35.2	9964	x	1	27.5	154529
	CAG	6.9	1948		8	12.2	68463
Glu	**GAA**	49.5	14001	x	3	45.9	257930
	GAG	11.5	3252		10	19.1	107568

TABLE 8 - continued

	C. albicans 522 CDS's					S. cerevisiae 11645 CDS's	
aa	codons	frequency: per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency: per thousand	total number
Gly	**GGU**	33.5	9492	x	2	23.9	134515
	GGC	4.5	1281		7	9.7	54629
	GGA	13.7	3874		2	10.9	61481
His	GGG	7.7	2182		8	6	33627
	CAU	14	3964			13.7	77260
	CAC	5.8	1642			7.8	43878
Ile	**AUU**	39.9	11281		3	30.2	169795
	AUC	14.2	4005	x	7	17.1	96126
	AUA	12.3	3478			17.8	100027
Leu	UUA	1	295			26.3	148133
	UUG	36.1	10204	x	2	27.1	152590
	CUU	9.8	2777		2	12.2	68479
	CUC	2.5	694		7	5.4	30218
	CUA	4	1133		1	13.4	75414
Lys	**AAA**	48.6	13760	x	2	42.1	236746
	AAG	19.4	5477		6	30.8	173174
Met	**AUG**	18.4	5219	x	8	20.9	117410
Phe	**UUU**	28.6	8100		4	26	146355
	UUC	15.9	4486	x	7	18.2	102389

TABLE 8 - continued

		C. albicans 522 CDS's				S. cerevisiae 11645 CDS's	
aa	codons	frequency: per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency: per thousand	total number
Pro	CCU	13.2	3722		1	13.6	76366
	CCC	3.6	1027		5	6.8	38247
	CCA	26.6	7531	x		18.2	102277
	CCG	2.4	686		1	5.3	29758
Ser	CUG	3.1	875		9	10.4	58583
	UCU	23.3	6595	x	1	23.6	132608
	UCC	10.3	2928		4	14.2	79928
	UCA	24.6	6955			18.8	105570
	UCG	6.5	1836		1	8.6	48186
	AGU	23.6	6673			14.2	79649
	AGC	4.5	1269		5	9.7	54330
Thr	ACU	30.7	8689		1	20.2	113634
	ACC	13.9	3928	x	8	12.6	70777
	ACA	17.4	4928		5	17.7	99759
	ACG	3.6	1019		1	8	44817
Trp	UGG	11	3115	x	6	10.3	58092
Tyr	UAU	24	6782			18.8	105489
	UAC	11.6	3280	x	2	14.7	82483
Val	GUU	33.2	9391		1	22	123726
	GUC	10.3	2927	x	3	11.6	65203
	GUA	8	2265			11.8	66100
	GUG	10	2842		7	10.7	60033

TABLE 9: Regulation of 23 selected "Bax-specific" functions

Cellular role: Amino-acid metabolism					
ORF	Gene	Control	Bax	H2O2	B vs C
YOR302W	YOR302W	11541.92	26806.35	8895.74	2.32
Cellular role: Cell stress					
ORF	Gene	Control	Bax	H2O2	B vs C
YML028W	TSA1	12889.91	2166.45	11327.36	0.17
Cellular role: Chromatin/chromosome structure					
ORF	Gene	Control	Bax	H2O2	B vs C
YBR009C	HHF1	2149.69	8655.43	2909.14	4.03
YDR224C	HTB1	13661.40	55656.34	18829.27	4.07
YNL030W	HHF2	8676.99	19603.93	4732.39	2.26
Cellular role: Energy generation					
ORF	Gene	Control	Bax	H2O2	B vs C
YBL099W	ATP1	2728.21	8786.71	1644.48	3.22
YGR183C	QCR9	23181.54	81865.40	24053.00	3.53
YJL166W	QCR8	5296.71	18093.93	5001.65	3.42
YLR038C	COX12	7336.65	19935.69	5118.43	2.72
Cellular role: Signal transduction					
ORF	Gene	Control	Bax	H2O2	B vs C
YHR135C	YCK1	3939.64	8358.11	3707.17	2.12
YOL100W	PKH2	2218.45	6088.96	2619.31	2.74
Cellular role: Transcription factor					
ORF	Gene	Control	Bax	H2O2	B vs C
YDR216W	ADR1	5925.91	18459.00	6434.43	3.11
Cellular role: Unknown					
ORF	Gene	Control	Bax	H2O2	B vs C
YDR504C	YDR504C	2741.47	6908.49	2839.62	2.52
YGR146C	YGR146C	2099.74	5616.94	1303.89	2.68
YGR236C	SPG1	17717.80	64439.96	24134.29	3.64
YHR138C	YHR138C	6218.30	14817.41	5220.50	2.38
YJL142C	YJL142C	6988.27	16006.02	6740.46	2.29
YKL123W	YKL123W	2826.82	5952.34	2766.04	2.11
YLR414C	YLR414C	4510.80	11867.69	3531.27	2.63
YMR107W	YMR107W	13453.15	78850.98	17417.00	5.86
YOL099C	YOL099C	3690.45	11604.72	5454.15	3.14
YPL201C	YPL201C	15960.14	33633.74	7449.66	2.11
YJL060W	YJL060W	8798.50	2406.39	6356.11	0.27

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CLAIMS

1. An isolated nucleic acid representing a synthetic *BAX*-gene selected from the group consisting of:
   a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,
   b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,
   c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,
   d) a nucleic acid which is more than 75 % identical to the nucleic acid as represented by SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c), and,
   e) a nucleic acid as defined in any one of (a) to (i) interrupted by intervening DNA sequences,
   or a nucleic acid representing the complement of any of said nucleic acids as defined in (a) to (d).
2. An isolated nucleic acid according to claim 1 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.
3. A vector comprising a nucleic acid as defined in claim 1 or 2.
4. A vector according to claim 3 which is an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
5. An expression vector according to claim 4 which comprises an inducible promoter
6. An expression vector according to claim 4 or 5 which comprises a sequence encoding a reporter molecule.
7. A vector according to any of claims 3 to 6 for inducing programmed cell death in *Candida* spp.
8. A host cell transformed, transfected or infected with a vector according to any of claims 3 to 7.
9. A host cell of claim 8 which is a bacterial, yeast or fungal cell.
10. A host cell according to claim 8 or 9 wherein said cell is a *Candida* spp. cell.
11. A genetically modified yeast or fungal cell according to claim 9 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

12. A genetically modified *Candida* spp. cell according to claim 10 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

13. A method for identifying Bax-resistant yeast or fungi comprising the steps of:

a) providing (a) genetically modified yeast or fungi according to claim 11,

b) treating said genetically modified yeast or fungi with a mutagen,

c) isolating resistant yeast or fungal cells, and,

d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.

14. A method for identifying *Candida* spp. sequences which are differentially expressed in a pathway eventually leading to programmed cell death using a nucleic acid as defined in claim 1 or 2, a vector according to any of claims 3 to 7 or a genetically modified host cell according to claim 10.

15. A method for obtaining and identifying *Candida* spp. sequences involved in a pathway eventually leading to programmed cell death comprising the steps of:

a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 1 or a vector according to any of claims 3 to 7 as a bait and a *Candida* spp. cDNA library as a prey are expressed,

b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide encoded by said cDNA library, and,

c) identifying said *Candida* spp. polypeptide or cDNA.

16. A method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:

a) providing a genetically modified organism according to claim 10,

b) expressing a cDNA library in said genetically modified organism, and,

c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.

17. A method according to claim 16 wherein said genetically modified organism is a *Candida* spp.

18. An isolated *Candida* spp. nucleic acid identifiable by any of the methods of any of claims 12 to 17.

19. An isolated *Candida* spp. nucleic acid according to claim 18 selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,

b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % similar to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % identical to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731,

e) a nucleic acid which is more than 70 % identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731, and

f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in any of a) to d),

20. An isolated nucleic acid as defined in according to claim 19 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.

21. An isolated nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 20 or the complement thereof.

22. An antisense molecule comprising a nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 21.

23. A nucleic acid probe which selectively hybridises with any of the nucleic acid molecules as defined in claim 18 or 19.

24. A nucleic acid primer which selectively amplifies any of the nucleic acid molecules defined in claim 18 or 19.

25. An expression vector comprising a nucleic acid according to any of claims 18 to 22.

26. An expression vector according to claim 25 which is an expression vector wherein said nucleic acid is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.

27. An expression vector according to claim 25 or 26 which comprises an inducible promoter.

28. An expression vector according to any of claims 25 to 27 which comprises a sequence encoding a reporter molecule.

29. A host cell transformed, transfected or infected with the vector of any of claims 25 to 28.

30. An isolated nucleic acid according to any of claims 18 to 22 for use as a medicament.

31. An isolated polypeptide which is involved in a pathway for programmed cell death of *Candida* spp. and encoded by a nucleic acid as defined in claim 18 or 19, wherein said polypeptide is selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a polypeptide having an amino acid sequence which is more than 70% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632,

634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and

(d) a functional fragment of any of said polypeptides as defined in a) to c).

32. A polypeptide according to claim 31 for use as a medicament.

33. An antibody capable of specifically binding to a polypeptide of claim 30 or to a specific epitope of said polypeptide.

34. An antibody according to claim 33 for use as a medicament.

35. A pharmaceutical composition comprising an antibody of claim 33 or 34.

36. Use of an isolated nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396,

398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562 ,564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415,

417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,

(e) a nucleic acid which is more than 70% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and

(g) the complement of any of the nucleic acid molecule as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

37. Use of an isolated polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,

(b) a polypeptide having an amino acid sequence which is more than 70% similar o any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302,

304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666,

668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said polypeptides as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

38. A pharmaceutical or fungicidal composition comprising a nucleic acid as defined in claim 36 or a polypeptide as defined in claim 37 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

39. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid as defined in claim 36 or at least one polypeptide as defined in claim 37 in a pharmaceutically acceptable carrier.

40. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or the polypeptides as defined in claim 36, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus.

41. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

(a) contacting a compound to be tested with a genetically modified yeast or fungus according to claim 40, in addition to contacting wild type cells with said compound,

(b) monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to said wild type cells; wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

(c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

(d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and,

(e) identifying the compound.

42. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

(a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid as defined in claim 36, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,

(b) monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

(c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

(d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and,

(e) identifying the compound.

43. A method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:

(a) contacting a compound or polypeptides to be tested with at least one of the polypeptides as defined in claim 37,

(b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide,

(c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound or polypeptide being tested,

(d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and,

(e) identifying the compound or protein.

44. A method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of:

(a) providing a two-hybrid screening system wherein a polypeptide of claim 37 and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method of claim 41, are expressed,

(b) interacting said compound with the complex formed by the expressed proteins as defined in a),

(c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and,

(d) identifying the compound.

45. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

(a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid as defined in claim 36 joined in frame with a reporter gene,

(b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and,

(c) identifying the compound.

46. A method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of:

(a) providing a two-hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 36 or a vector according to any of claims 3 to 7 as a bait and a yeast or fungal cDNA library as a prey are used,

(b) detecting an interaction between said polypeptide and a yeast or fungal polypeptide encoded by said cDNA library, and,

(c) identifying said yeast or fungal polypeptide.

47. A method according to any of claims 41 to 46 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

48. A compound or polypeptide identifiable according to the method of any of claims 41 to 47.

49. A compound or polypeptide according to claim 48 for use as a medicament.

50. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound or polypeptide according to claim 49 with a suitable pharmaceutically acceptable carrier.

51. A pharmaceutical composition comprising a compound or polypeptide according to claim 49 together with a suitable pharmaceutically acceptable carrier.

52. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or obtainable by the method of claim 50 for the preparation of a medicament for treating diseases associated with yeast and fungi.

53. A method for preventing infection with yeast or fungi comprising administering a composition according to claim 51 or obtainable by the method of claim 50 to a mammal in an effective amount to stimulate the production of protective antibody or protective T-cell response.

54. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a specific epitope of said polypeptide, for the preparation of a medicament for treating diseases associated with yeast and fungi.

55. Use according to any of claims 52 to 54 wherein said disease is associated with yeast or fungi, where the yeast or fungus is chosen from *Candida* spp., Aspergillus spp., Microsporum spp., Trichophyton spp., Fusarium spp., Zygomycetes spp., Botritis, spp., Cladosporium spp., Malassezia spp., *Epidermophyton floccosum, Blastomyces dermatitidis, Coccidioides immitis, Histoplasma capsulatum, Paracoccidioides brasiliensis, Cryptococcus neoformans*, and *Sporothrix schenckii.*

56. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or a genetically modified organism as defined in claim 40 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

57. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof or at least one of the polypeptides as defined in claim 37 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

58. A genetically modified mammalian cell or non-human organism according to claim 57 wherein said modification comprises the expression of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid.

59. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 37 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 57 or 58.

60. A compound identifiable according to the method of claim 59.

61. A compound according to claim 60 for use as a medicament.

62. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 60 or 61 with a suitable pharmaceutically acceptable carrier.

63. Use of a compound according to claim 60 or 61 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

64. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for treating an/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.

65. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.

66. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.

67. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.

68. Use of a polypeptide selected from any of the polypeptides as defined in claim 37 or a human homologue thereof for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.

69. A pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 36 or a human homologue thereof or an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid or a polypeptide as defined in claim 37 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.

70. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid as defined in claim 36 or a human homologue thereof or at least one polypeptide as defined in claim 37 or a human analogue thereof in a pharmaceutically acceptable carrier.

71. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue, for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

72. An expression vector comprising a human homologue of a nucleic acid as defined in claim 36.

73. An expression vector according to claim 72 which is an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.

74. An expression vector according to claim 72 or 73 which comprises an inducible promoter.

75. An expression vector according to any of claims 72 to 74 which comprises a sequence encoding a reporter molecule.

76. A host cell transformed, transfected or infected with the vector of any of claims 72 to 75.

77. An isolated nucleic acid comprising a human homologue of at least one of the nucleic acids as defined in claim 36.

78. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 77.

79. A polypeptide encoded by a nucleic acid of claim 77.

Figure 1:

YBL002W, 896 bp, CDS: 501-896 (SEQ ID NO 21)
TGTTTGATATTAGTAGTCATGTTGTAATCTCTGGCCTAAGTATACGTAACGAAAATGGTA
GCACGTCGCGTTTATGGCCCCCAGGTTAATGTGTTCTCTGAAATTCGCATCACTTTGAGA
AATAATGGGAACACCTTACCCCTGAGCTGTGCCCACCGCTTCGCCTAATAAAGCGGTGTT
CTCAAAATTTCTCCCCGTTTTCAGGATCACGAGCGCCATCTAGTTCTGGTAAAATCGCGC
TTACAAGAACAAAGAAAAGAAACATCGCGTAATGCAACAGTGAGACACTTGCCGTCATAT
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ATATATCATGGTATATGTGTAAAATTTTTTTGCTGACTGGTTTTGTTTATTTATTTAGCT
TTTTAAAAATTTACTTTCTTCTTGTTAATTTTTTCTGATTGCTCTATACTCAAACCAAC
AACAACTTACTCTACAACTAATGTCCTCTGCCGCCGAAAAGAAACCAGCTTCCAAAGCTC
CAGCTGAAAAGAAGCCAGCTGCCAAGAAAACATCAACCTCCGTCGATGGTAAGAAGAGAT
CTAAGGTTAGAAAGGAGACCTATTCCTCTTATATTTACAAAGTTTTGAAGCAAACTCACC
CAGACACTGGTATTTCCCAGAAGTCTATGTCTATTTTGAACTCTTTCGTTAACGATATCT
TTGAAAGAATTGCTACTGAAGCTTCTAAATTGGCCGCTTATAACAAGAAATCCACTATTT
CTGCTAGAGAAATCCAAACAGCCGTTAGATTGATCTTACCTGGTGAATTGGCTAAACATG
CCGTCTCCGAAGGTACTAGGGCTGTTACCAAATACTCCTCCTCTACTCAAGCCTAA

YBL002W, 131 aa(SEQ ID NO 22)
MSSAAEKKPASKAPAEKKPAAKKTSTSSVDGKKRSKVRKETYSSYIYKVLKQTHPDTGISQ
KSMSILNSFVNDIFERIATEASKLAAYNKKSTISAREIQTAVRLILPGELAKHAVSEGTR
AVTKYSSSTQA

YBL064C, 1286 bp, CDS: 501-1286 (SEQ ID NO 25)
TTGCCAACCTCAAAGAAGAAGAATTATGGGCATATTGACCTTCTCCGGTTTCCCTCCCGC
GCTCTCGTATCCGTCTGCATTTGACCTCGAGCAAGCGCTCCACTATGTCTATATGTTTAC
CAGTAAAACTTCTTAACGTTTGTGATATTTTTTGAACTTCAACCACATTCAGTATGCGTG
TGTATATAAAGATATTCCTGATAGCACTATGTTTATCTTTATACAATATACAAAAGGTCA
CCCAGGACGAGCAGCGCGGCTATTTTTCTATCATTCCGTGAATAGCGACCAACGGTCGGC
GGCTATTTTTTTTTTTGCAATTTTTTCGGGATGGGTTCCCCGGCAAAAGCTAGCCCCGGA
GATTTTTAATTACGTAAAGAAACAAGGGGCCGGATGTTGCTGCTATTGGTATATAAAGAG
AGAAGGAGAGATATAGAAAATTGTGCTTCTAGATTCTCGCAGTAGGATGAGATAAATTTC
AAAGAAGCAGGAAGCAAAGGATGTTTAGTAGAATTTGTAGCGCTCAATTAAAGAGGACGG
CATGGACCCTTCCTAAGCAGGCTCACTTGCAATCACAGACGATTAAAACATTTGCCACAG
CACCTATTCTGTGCAAACAATTCAAACAAAGTGATCAACCAAGACTAAGAATAAACTCTG
ATGCTCCTAACTTTGATGCTGACACAACGGTTGGTAAAATCAATTTTTACGACTACTTGG
GCGACTCTTGGGGGGTCTTGTTTTCTCACCCAGCAGATTTCACCCCTGTCTGCACCACCG
AAGTCAGCGCATTCGCCAAATTGAAGCCGGAATTCGACAAGAGAAATGTTAAATTGATCG
GGCTTTCAGTGGAAGATGTTGAGTCCCACGAAAAATGGATTCAAGACATCAAGGAAATAG
CAAAGGTTAAAAATGTTGGTTTCCCAATAATTGGTGACACTTTTAGAAACGTGGCATTCC
TATATGATATGGTAGATGCCGAAGGATTCAAAAATATCAATGATGGGTCACTGAAGACCG
TGAGGTCTGTTTTCGTCATCGATCCCAAGAAGAAGATTAGACTGATTTTTACCTACCCTT
CCACCGTCGGAAGAAACACTTCTGAAGTGTTAAGGGTAATCGACGCCTTGCAATTGACTG
ACAAGGAGGGCGTAGTAACTCCAATTAATTGGCAGCCAGCTGACGATGTCATTATTCCTC
CCTCTGTCTCCAATGATGAGGCGAAGGCTAAATTTGGTCAATTTAATGAAATTAAACCCT
ATTTAAGATTCACCAAGTCGAAATAA

YBL064C, 261 aa (SEQ ID NO 26)
MFSRICSAQLKRTAWTLPKQAHLQSQTIKTFATAPILCKQFKQSDQPRLRINSDAPNFDA
DTTVGKINFYDYLGDSWGVLFSHPADFTPVCTTEVSAFAKLKPEFDKRNVKLIGLSVEDV
ESHEKWIQDIKEIAKVKNVGFPIIGDTFRNVAFLYDMVDAEGFKNINDGSLKTVRSVFVI
DPKKKIRLIFTYPSTVGRNTSEVLRVIDALQLTDKEGVVTPINWQPADDVIIPPSVSNDE
AKAKFGQFNEIKPYLRFTKSK

YBR089C-A, 800 bp, CDS: 501-800 (SEQ ID NO 47)

TTTTTTAGGTGGCGCGGCAACTATAAAGTACAGCAAGTGAGGTTGAGGCAATACTGGGAG
TTTACACTATGGGAGACAGCTCCTAACACCAAGCAGAAAAACGACTTTTTCGCAAAGTAT
GTAAGGCGCTGGGTGAGCCCAGCGGACGAGGATGGGCTTAATAAGAACGTACAGTTTAGC
ACAGCTAGAACAGGATACAGCTAAGGGCAACTCTGCTTTTCGGGAGAAGTTAAAGAGGGG
TAGACAATGATGGTAATCTTATAAACCGGCTACAATGAAGGTTGTAGCAGCAAGGAAGAT
GATATTTTAATACGGTTCAGGTGAAATGAAATAGCCGCCCATAACGGCATGCTCAAGTTG
TAAGTCAGGACTCTAGCTTTCTACTGTAGTATCCTCTAAAGGACTGCTGTTCTGTGCACC
CCCTTCCTTTGTTTATCATAGCGCACGACAAGAGTACTAACTAATTAACTTAGAACATTA
ACATATATAAAACTAGCGCTATGGCCGCAACTAAAGAAGCAAAGCAACCAAAGGAACCAA
AGAAGAGGACCACCAGGAGAAAGAAGGATCCTAACGCCCCTAAGAGGCGGTTGTCAGCTT
ATATGTTCTTTGCTAATGAAAACAGAGACATTGTCCGTTCCGAGAATCCTGACGTAACTT
TTGGCCAAGTAGGCAGAATATTGGGTGAGAGGTGGAAGGCCTTAACTGCTGAAGAAAAGC
AACCCTATGAATCTAAGGCTCAAGCAGACAAGAAGAGATACGAATCTGAAAAGGAATTGT
ACAATGCTACACGTGCTTGA

YBR089C-A, 99 aa (SEQ ID NO 48)

MAATKEAKQPKEPKKRTTRRKKDPNAPKRRLSAYMFFANENRDIVRSENPDVTFGQVGRI
LGERWKALTAEEKQPYESKAQADKKRYESEKELYNATRA

YBR149W, 1535 bp, CDS: 501-1535 (SEQ ID NO 57)

TTCGCAAACATCAACTTCTCCTTAATCGACCAACTGACAATGAACTTCAGGTTCTACGAG
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TAAAAACTCGTTTATTGCCGATTATAAATCCACCAAAAGCCGCTCTACCCTTACCTCCGC
CTGGAAAAATTATAATATATAAAGTGAGCCTCGTAATACAGGGGTAAAAAGGAAAGAGGG
GGATATCAAGCATCTGGACTTATTTGCACTATCTCCGCCTTCAATTGATAAAAGCGTCTT
GATTTTAATCAACTGCTATCATGTCTTCTTTCAGTAGCCTCAACCGAAAACATAGTCGAAA
ATATGTTGCATCCAAAGACTACAGAAATATACTTTTCACTCAACAATGGTGTTCGTATCC
CAGCACTGGGTTTGGGGACAGCAAATCCTCACGAAAAGTTAGCTGAAACAAAACAAGCCG
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ATGAATCTTTGAAAGCTTTAGGCTTGGAATACGTCGACTTGCTCTTGCAACATTGGCCGC
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CACTAGTGAAAAAGCTTGCCGAAAAGTACAATGTCACAGGAAATGACTTGCTAATTTCTT
ACCATATTAGACAAGGCACTATCGTAATTCCGAGATCCTTGAATCCAGTTAGGATTTCCT
CGAGTATTGAATTCGCATCTTTGACAAAGGATGAATTACAAGAGTTGAACGACTTCGGTG
AAAAATACCCAGTGAGATTCATCGATGAGCCATTTGCAGCCATCCTTCCAGAGTTTACTG
GTAACGGACCAAACTTGGACAATTTAAAGTATTAA

YBR149W, 344 aa (SEQ ID NO 58)

MSSSVASTENIVENMLHPKTTEIYFSLNNGVRIPALGLGTANPHEKLAETKQAVKAAIKA
GYRHIDTAWAYETEPFVGEAIKELLEDGSIKREDLFITTKVWPVLWDEVDRSLNESLKAL
GLEYVDLLLQHWPLCFEKIKDPKGISGLVKTPVDDSGKTMYAADGDYLETYKQLEKIYLD
PNDHRVRAIGVSNFSIEYLERLIKECRVKPTVNQVETHPHLPQMELRKFCFMHDILLTAY
SPLGSHGAPNLKIPLVKKLAEKYNVTGNDLLISYHIRQGTIVIPRSLNPVRISSSIEFAS
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YBR289W, 3218 bp, CDS: 501-3218 (SEQ ID NO 63)

GATACGATCTATAGTCTCTAAAAAGGTAAAACAATCAAGCGGGCCTTTTGACTTCGAAGT
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AGGACATGTGGTACGAACGCGGGTCCACAGGTGCTTGAAGGAGGGAGCTGTTGCACCTAA
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GGGACACTTTGTTATGGAACAAAAATGACAAGCTTATTAAAATTGAAGACTTTGTGGACG
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AAGTTAATACAAAAGAAGAGTTCGCAGCAGCGCCCAATGACACAAGTAGTGGCACCAATG
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YBR289W, 905 aa (SEQ ID NO 64)

MNNQPQGTNSVPNSIGNIFSNIGTPSFNMAQIPQQLYQSLTPQQLQMIQQRHQQLLRSRL
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LPKLNLPKYQTIQYDPPETKLPYPTYWSDKKADTDTLLYEQIIQRDKINKYSLIRETNGY
DPFSIYGFSNKEYISRLWHTLKYYQDLKNTRMKSITSTSQKIPSASIWGNGYSGYGNGIT
NTTTRVIPQVEVGNRKHYLEDKLKVYKQAMNETSEQLVPIRLEFDQDRDRFFLRDTLLWN
KNDKLIKIEDFVDDMLRDYRFEDATREQHIDTICQSTQEQIQEFQGNPYIELNQDRLGGD
DLRIRIKLDIVVGQNQLIDQFEWEISNSDNCPEEFAESMCQELELPGEFVTAIAHSIREQ
VHMYHKSLALLGYNFDGSAIEDDDIRSRMLPTITLDDVYRPAAESKIFTPNLLQISAAEL
ERLDKDKDRDTRRKRRQGRSNRRGMLALSGTSASNTSMNGVHNTVAAGNASSLPPGEILL
PDIADIPRTFRTPVPSTLMPGQVDVGPSVESYELRNTTTYKSRPDRPKPVSPPCYIIDHI
PGHSLLLSIKLPGKVNTKEEFAAAPNDTSSGTNAMLPSPESLKTKLNSNIRAGVTIPSIP
NPIANHTVTNSPNPTLQPVIPGGAASKSVPTPSLPIAPPVAPHDSEATLLTNSNNGSSNN
NTQNT

YCR004C, 1244 bp, CDS: 501-1244 (SEQ ID NO 69)

TTAAGAAAATGAACGTTACTATTTCCTTCCTCGTTTTAGTTACATAAAATTTACTAATGG
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AATTTGCCTAAGGGCATTAGGCCTTACTGCCTTGGCTAGCGTACTTATTTCGATTCATAC
AATTTGCACTATTCCGGCAGCTAGTTGATACTATAACATCCTACATTTTTACTTGTTTTA
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CTCATCACGGAATTATCTTTTTACCACTGGGTTATAAGAATTCATTTGCTGAGTTAGCCA
GTATAGAAGAGGTACACGGTGGCTCTCCATGGGGTCGTGGTACCCTTGCAGGACCTGACG
GCTCAAGAACTGCGTCTCCACTTGAATTGAGAATTGCTGAAATTCAAGGTAAAACATTCT
ACGAAACCGCCAAAAAACTTTCCCTGCAAAAGAAGCCAAGCCCTCCACTGAAAAGAAGA
CCACTACTTCTGATGCGGCTAAGAGACAAACTAAACCTGCAGCAGCTACAACTGCAGAAA
AGAAGGAGGACAAAGGATTATTATCCTGCTGTACTGTCATGTAA

YCR004C, 247 aa (SEQ ID NO 70)

MVKIAIITYSTYGHIDVLAQAVKKGVEAAGGKADIYRVEETLPDEVLTKMNAPQKPEDIP
VATEKTLLEYDAFLFGVPTRFGNLPAQWSAFWDKTGGLWAKGSLNGKAAGIFVSTSSYGG
GQESTVKACLSYLAHHGIIFLPLGYKNSFAELASIEEVHGGSPWGAGTLAGPDGSRTASP
LELRIAEIQGKTFYETAKKLFPAKEAKPSTEKKTTTSDAAKRQTKPAAATTAEKKEDKGL
LSCCTVM

YCR013C, 1148bp, CDS: 501-1148 (SEQ ID NO 77)

TGAAAAATGATGAAGGCACATTGTTAATTGAAGAAGAAGAAGAAGAAGAAACAAAATTAA
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AAGAGTACAATAGATGGATAAGAATATTGGCAGCGCAAAAAGGCTTCAAGCTTACACAAC
ACGGTTTATTTCGAAATAATATCCTTCTCGAAAGCTTTAACGAACGCAGAATTTTCGAGT
TATTAAACTTAAAATACGCTGAACCCGAACATAGAAATATCGAATGGGAAAAAAAAACTG
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AGATAAATAATAGTCTATATATACGTATATAAATAAAAAATATTCAAAAAATAAAATAAA
CTATTATTTTAGCGTAAAGGATGGGGAAAGAGAAAAGAAAAAAAATTGATCTATCGATTTC
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CCAATAATTCCAAAGAAGCACCACCACCAGTAGAGACATGGGAGATCTTGTCAGTGACAC
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CAGAGCTCTTGACAACTTCGTCTAACAAAGCCTTAGTACCAGCAGCGAACTTTTCGAATT
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ACAACTTTCTAGATTCTGGACCATTGTCCAACCCTTGCCAGCCAGCTGGAATACCTTCCT
TGTCAGTGACAGTCTTGGTGTTGGCATCAGCAGAGAAAGCATCAGCAATGATGAAGTCGA
CTGGCAAGACGACTTCGACACCCTTGGCCTTGGCCTTTTCCATCAACTTTGGAACGATTT
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AGGTGAAAGCCATACCACCACCAATGATGATAGAGTCGACCTTGTCCAACAAGTTGTCAA
TCAATTGA

YCR013C, 215 aa (SEQ ID NO 78)
MGKEKRKKLIYRFQFNSIYFFSDKKATPGNSLPSNNSKEAPPPVETWEILSVTPYFLATV
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PLSNPCQPAGIPSLSVTVLVLASAEKASAMMKSTGKTTSTPLALAFSINFGTISAPALSK
MESPISVFSKTFLKVKAIPPPMMIESTLSNKLSIN

YDL059C, 1217 bp, CDS: 501-1217 (SEQ ID NO 83)
AAAGTATCAAGTTCGCTAAATTTACTTCGAAGACAGAAGCCAGTAAATTTTGTTTTCTTC
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GAAAGAAAGGTTAGCCGACCGGCATCACCCATAATTGTATAATATAGCAATGAAGCAACT
TGTTGAAGTTTTCTTTAAAGTACTATAGTATTGAATAATATCATGTTCACTTGATAAAAT
TGGGTATTTTATTGACCATTATATCGCGTTGGACACTAATGTCTTTCAAGTTGGTGTCAC
GTCACGTGCTTTTCAATGTACTGGGGCAAATTGATTAGAGGAAGCCACAGTTTGGCAAGG
GCAGATATGATAGGAAGCAGTAACGGCAAGGAAGGATAAGAACATCATTGAGGAGTCTG
TGGCAGTTTAGCACATGCTTTGGACCATTAAAGGGTTACGTAGAGGAGAAGAGCATATTT
CAGGATAAACAGACAAAATAATGACGATACAAGCGAAGCCCAGTTCGAGCATATCGTATG
ATTCGACTACATACGGCACAGCACCGGGCTTGGATATAAAAGAGTTCCAAATCATCGAAG
ATTGGAATGGAAGACCTGCCAGCGCTTGGTCGGTGCAGAGGATTGGGCTTCTACAGTCCA
AGATCGAAAGGTACACGTACAATATTTACCACAATAATAAATATGGGAAGCACAACTTAT
CTAAGCTGATACCAGGGCATGCTCTCATTCAGTTCGCTAATGAAACATTCGGGTATGATG
GTTGGCGAATGGATGTTATAGATGTTGAGGCCCGGGAGTGCCAGCCCTTCACCGCAGTAA
ATAATGGAGAAAACACCAACACTAGTGAGGTCAAGTATACAGTTGTGGCAGAAGCCCAAG
TAAAGGTTACCTTAAAGGATGGCACCAACACACAGTGTGGTGGGCTAGGTAGAATTACTT
TGTCCTCGAGAGGTGAATGTTATAACAGGTCGAAAAAAGAGGCTGTAGGCGATGCGTTAA
AGAAGGCGTTATTGAGCTTTGAAAAAATCATACTCGATTATGAGACTAAGATTACAAATA
ATTACTATGTCGATGGCTTCTATGGCTCAAAAAAAATTAAAAATGAAGCTAACACCAATT
ACAACTTATTGTCAGCGACTAATAGCAAGCCGACTTTTATCAAATTGGAGGATGCTAAAG
GCACGCATATCAAATAA

YDL059C, 238 aa (SEQ ID NO 84)
MTIQAKPSSSISYDSTTYGTAPGLDIKEFQIIEDWNGRPASAWSVQRIGLLQSKIERYTY
NIYHNNKYGKHNLSKLIPGHALIQFANETFGYDGWRMDVIDVEARECQPFTAVNNGENTN
TSEVKYTVVAEAQVKVTLKDGTNTQCGGLGRITLSSRGECYNRSKKEAVGDALKKALLSF
EKIILDYETKITNNYYVDGLYGSKKIKNEANTNYNLLSATNSKPTFIKLEDAKGTHIK

YDL147W, 1838 bp, CDS: 501-1838 (SEQ ID NO 87)
ACTCTTCTCTGATTTCAGCAATGGCCTTTTTTTTTTTCTTCACGATCATACTCCTTCGCTT
GTCTTTTGGAATTCTTTTTATTCTTACTTTTGACGTTTGTTTGACCTGTGAGTCCACGGG
CCTTCAAGGCGGCCTTTAAATTCTTAAGTTGTGAACCGGCCATGTATTTGATCTTCCCTT
TTATTTGCTTCTCAACTGTACTATTTACAGTAATAATTAGTGCAACCTTCAGATGCTTCT
CGCTAAATGCTCATCTCTAAATTATCATTATTATTCCTAATAAATCCTAAAATTTTTCAC
TCGTTCTGTACGGCTCATCGCCCCAATATTACCCGTCTTGTATGTGATCTTTTTGACTTT

TCGGTGGCAAAATGCAAAGGGGAATCCAAGGAAAAACCATAACAGGACACTACATCAGAG
ATAATCTTGAATTAAGAGAGTAGAGGAATATACTGCTGGGCTCACTACCATTTTTGTTGC
TAGAGTAAACGTAGAGAAAGATGTCAAGAGATGCACCAATTAAGGCTGACAAGGATTATA
GCCAAATTTTGAAGGAAGAGTTTCCTAAGATCGATTCGCTCGCTCAAAATGATTGTAACT
CTGCTTTAGACCAACTGTTAGTGTTGGAGAAGAAAACCAGACAAGCTTCAGATCTGGCCT
CCTCGAAAGAAGTTTTGGCCAAGATTGTAGATCTGCTAGCATCAAGGAATAAGTGGGACG
ACCTAAATGAGCAATTGACTCTACTCTCAAAAAAGCATGGTCAGTTGAAATTGTCAATTC
AGTATATGATACAAAAGGTTATGGAATATTTGAAAAGCTCGAAATCTTTGGATTTAAACA
CCAGAATTAGTGTCATTGAAACTATCAGGGTGGTTACAGAGAACAAAATATTTGTAGAAG
TGGAAAGAGCTAGGGTCACCAAAGATTTGGTGGAAATTAAGAAAGAAGAGGGTAAGATTG
ATGAAGCTGCAGACATCTTGTGTGAGTTACAGGTTGAGACCTATGGCTCCATGGAAATGT
CTGAGAAAATTCAGTTTATATTAGAGCAAATGGAATTGAGTATATTAAAAGGTGATTATT
CCCAAGCCACGGTGCTTTCAAGAAAAATTCTGAAAAAAACTTTAAAAATCCAAAATACG
AGTCATTGAAGCTAGAATATTATAATCTTCTGGTAAAAATTAGTTTGCACAAGAGAGAAT
ACCTAGAAGTTGCGCAGTATCTGCAAGAAATTTATCAAACAGACGCCATTAAATCAGATG
AGGCTAAGTGGAAACCTGTTTTATCGCACATTGTATATTTCTTAGTCCTTTCACCTTACG
GCAATTTACAAAATGATTTAATTCACAAAATCCAGAATGATAACAACCTGAAAAAATTAG
AAAGCCAAGAATCTTTAGTAAAATTGTTTACTACGAATGAGTTGATGAGATGGCCAATTG
TTCAAAAAACCTATGAGCCCGTCTTAAATGAGGATGATTTGGCATTTGGTGGAGAAGCTA
ATAAGCATCACTGGGAAGATTTACAAAAAAGGGTCATCGAGCACAATTTAAGAGTCATTT
CCGAATACTATTCCAGAATTACTTTACTAAGATTGAATGAATTGCTGGACCTAACGGAGA
GCCAGACGGAAACATACATCAGTGATTTGGTAAACCAGGGCATCATATACGCTAAAGTTA
ATCGCCCAGCCAAAATCGTGAATTTTGAAAAACCAAAAAACTCAAGCCAATTATTGAACG
AATGGTCACATAATGTTGACGAACTATTAGAACATATAGAAACAATAGGCCATTTAATTA
CAAAAGAGGAAATCATGCACGGTTTGCAAGCTAAATGA

YDL147W, 445 aa (SEQ ID NO 88)
MSRDAPIKADKDYSQILKEEFPKIDSLAQNDCNSALDQLLVLEKKTRQASDLASSKEVLA
KIVDLLASRNKWDDLNEQLTLLSKKHGQLKLSIQYMIQKVMEYLKSSKSLDLNTRISVIE
TIRVVTENKIFVEVERARVTKDLVEIKKEEGKIDEAADILCELQVETYGSMEMSEKIQFI
LEQMELSILKGDYSQATVLSRKILKKTFKNPKYESLKLEYYNLLVKISLHKREYLEVAQY
LQEIYQTDAIKSDEAKWKPVLSHIVYFLVLSPYGNLQNDLIHKIQNDNNLKKLESQESLV
KLFTTNELMRWPIVQKTYEPVLNEDDLAFGGEANKHHWEDLQKRVIEHNLRVISEYYSRI
TLLRLNELLDLTESQTEIYISDLVNQGIIYAKVNRPAKIVNFEKPKNSSQLLNEWSHNVD
ELLEHIETIGHLITKEEIMHGLQAK

YDR253C, 1076 bp, CDS: 501-1076 (SEQ ID NO 113)
TTTCCCCGCTAAAATAACGCCAGATGCTTTCTATGCTTCTAATCTTTTACCATTTACCTT
TGTTTATTTCAATATAAACTTTAATTTACAGTCCCTATCTATTGCCCGACTGGACTAACA
TGCACGTGACATTTTGTGATGGTTTTTCGTCCCTTACTTAGTACGCTTAGTACGCCACAG
TTTATATTTTCTTGACAATAATAAAGAACCTGATTGTGGGTTAGAACTTGCTATACTTTT
AGTTTAAAATAAGCAGGAAATAATCTTGAGTTCTGTATCATTATTATAAATAAAACTATA
TTTGTTCTCTTTGTCGCCCTCGGAACTTTCCTCATTACATTGACGAGGTATATATAGATA
TAGTAGATATACATATCTATCCATGGTATATATGTATGCATCTGGATAATTGAATAGGGT
TTCATGTCATATGCCAAGAATTTGTTAATAATATAGTGGAAAAAAGTCAAGAGGTATTAT
AAATTTCAAAAAAGTACCAAATGGAGGATCAGGATGCTGCATTTATCAAACAGGCTACAG
AAGCAATAGTGGATGTATCATTAAATATAGATAACATAGATCCTATAATAAAAGAGTTAT
TAGAAAGGGTAAGGAATAGGCAAAACAGGTTACAAAATAAAAAACCAGCACTCATACCGG
CAGAAAATGGTGTTGATATAAATAGTCAAGGCGGTAACATAAAGGTTAAAAAGGAAAACG
CATTACCAAAACCACCGAAGTCCAGCAAAAGCAAACCCAAGATCGTAGAAATAGTACTG
GTGAAAAAAGATTTAAATGTGCGAAATGTTCGTTGGAATTTTCAAGATCATCAGATTTGA
GAAGGCACGAAAAGACACACTTCGCCATATTGCCTAACATTTGTCCTCAATGTGGCAAAG
GTTTTGCAAGGAAAGATGCATTGAAAAGACATTATGATACACTGACATGTAGGAGAAACA
GGACTAAATTACTAACTGCGGGTGGTGAGGGTATCAATGAATTACTGAAAAAAGTCAAGC
AATCCAACATCGTTCATCGTCAAGATAACAACCACAATGGTAGCAGTAATGGCTGA

YDR253c, 191 aa (SEQ ID NO 114)
MEDQDAAFIKQATEAIVDVSLNIDNIDPIIKELLERVRNRQNRLQNKKPALIPAENGVDI
NSQGGNIKVKKENALPKPPKSSKSKPQDRRNNSTGEKRFKCAKCSLEFSRSSDLRRHEKTH
FAILPNICPQCGKGFARKDALKRHYDTLTCRRNRTKLLTAGGEGINELLKKVKQSNIVHR
QDNNHNGSSNG

YDR276C, 668 bp, CDS: 501-668 (SEQ ID NO 117)
ACCTTTAGTTCTTAGCATCACCAATCGCAGACATCCAACGTATCCGTGCGCGTAATCCTT
CTCTTGGTAGTTGAGCACAGCATACAGAAGAAGCCGCGCGCAAGCGGTAAATGTCTTTCC
TCCGGCCTTCTAACCACCAAAACCGATCTCGGAACATGGGGGGGGGAAGGTCCTCTGAAT
CGAAAAACCCGAGACAGCGAGAGGGATTTTGCAGAAAATTACAAAGATCACTATTTACTG
CTCCCCTCACTTCCGCAGTCCCCTAATAGCGGAAGATGCAATGGGTGTGGGCTCTGGGTG
CCCTTTAACCACGCCCTCAAAAGGGGGTCCTGGTTATTTTGCGATGGGCGCCTCTATAAA
TACAAAAGAGGAAGTGAGTGTTTTTGTTTTGGAAGAGGGAAAGGAAAAAAAGAAGAAAAT
TTACTATCGGTTGTTGTTTTTCGCCAGTATAATACAATTGATTATACATTTTGAACTAAA
CAGCACAGCACAATACAACAATGGATTCTGCCAAGATCATTAACATTATATTATCCCTTT
TCTTACCACCAGTCGCCGTTTTTCTAGCCCGTGGGTGGGGTACTGACTGTATAGTGGATA
TCATTTTGACCATTTTGGCTTGGTTCCCAGGTATGCTATATGCCTTGTACATTGTCCTAC
AAGATTAA

YDR276C, 55 aa (SEQ ID NO 118)
MDSAKIINIILSLFLPPVAVFLARGWGTDCIVDIILTILAWFPGMLYALYIVLQD

YDR377W, 806 bp, CDS: 501-806 (SEQ ID NO 127)
AATACAAGACTTGGTGGTCAGCGGAGCGCTATCCTTAGAGAATTCTATCGACCTCTCTAA
TATCAAGCACACCACATGGAAGGATTGGGAAAGAATCAACAAGAAGGAATTGCTTCGGGG
CAAAAAGGAACACAAAACTCGGTCAAAGTTTTTAACTTTTGAAGAGTTGTGGAACGGTGT
AGAAGGCATATAAAATAGATCGTTAATATATTTCTAACATCTTCTTGTAAATGTAAATAT
TTTAAAAGGGTTGATCTTATTACGGAGAGAACCAATCATATCGAAGGATTTCTCAATAGT
AAGTATCCCGCGCGTGGTCCTCGGGGAAATAGAACGAGAAACTTCAAGTACTTGATAGCA
AGAAAGTGAGTGCTTGGCTTCCCCATTTTGATTATAAAGAAAGGCATTATTTTCTAGGGC
AAGAAAAGACATTGTTGAAATTGTTCCAGAAACTTTCATTTAAAGTCTTTCGTGAAAGGA
GTGGACGTCAAAAAGAAATAATGATTTTTAAACGTGCAGTATCTACATTGATTCCTCCAA
AAGTTGTGTCTTCCAAGAATATAGGTTCGGCACCAAATGCCAAGCGCATTGCTAATGTTG
TTCACTTTTATAAGTCTTTGCCTCAAGGACCAGCACCAGCCATCAAGGCTAACACTAGAT
TGGCCAGATACAAAGCCAAGTACTTTGATGGGGATAATGCTAGTGGTAAACCATTGTGGC
ATTTTGCTCTAGGTATAATTGCCTTTGGCTATTCCATGGAATATTATTTTCATTTGAGAC
ATCATAAAGGTGCGGAAGAGCATTGA

YDR377W, 101 aa (SEQ ID NO 128)
MIFKRAVSTLIPPKVVSSKNIGSAPNAKRIANVVHFYKSLPQGPAPAIKANTRLARYKAK
YFDGDNASGKPLWHFALGIIAFGYSMEYYFHLRHHKGAEEH

YEL039C, 842 bp, CDS: 501-842 (SEQ ID NO 141)
AGTAATTGTCTCCCATTTTTGGTATACGAGCTAGCAGGACCTTTTGCCCAATGACCATTC
CATATTCATCCCACTCACCACCGTCATCGTTGGTATTATTATTATCATTCCGCTTGAAGA
AAAAGAAACGAAAAAAGAAATGGATCAGCAGCCGGGTTATAGCGCCCCTTATTGAATTAT
TTTCCTTCGTGCCTTCTCTGAGAAGGGTCTGCAGTCCCCCGCCGAGGGGTCTTTTCCCAC
CTTCTCAAAGCTAATAGCGATAATAGCGAGGGCATTTATTCAAGTTCCAACTACTATAAG
TGGCCGCAAGGGGCAAAGACAAAGGCACACAACATATATATATCGTGTTGTGAAGCTC
GAGAAGATTAGATCAGAATAGTTCTCTTTTTGTTGAGGTTGAAACAAAATCAAAGACTTA
TACAAGAAGATCACATACAAGCATTTATTCACATTACTTTAAGTAAACTTCAGTAAACTA
CATTACATCATAAACAAAACATGGCTAAAGAAAGTACGGGATTCAAACCAGGCTCTGCAA
AAAAGGGTGCTACATTGTTTAAAACGAGGTGTCAGCAGTGTCATACAATAGAAGAGGGTG
GTCCTAACAAAGTTGGACCTAATTTACATGGTATTTTTGGTAGACATTCAGGTCAGGTAA
AGGGTTATTCTTACACAGATGCAAACATCAACAAGAACGTCAAATGGGATGAGGATAGTA

TGTCCGAGTACTTGACGAACCCAAAGAAATATATTCCTGGTACCAAGATGGCGTTTGCCG
GGTTGAAGAAGGAAAAGGACAGAAACGATTTAATTACTTATATGACAAAGGCTGCCAAAT
AG

YEL039C, 113 aa (SEQ ID NO 142)
MAKESTGFKPGSAKKGATLFKTRCQQCHTIEEGGPNKVGPNLHGIFGRHSGQVKGYSYTD
ANINKNVKWDEDSMSEYLTNPKKYIPGTKMAFAGLKKEKDRNDLITYMTKAAK

YER112W, 1064 bp, CDS: 501-1064 (SEQ ID NO 147)
TACTGAAGTCCCTCTAAACCTACTGCCTTTTATTTTTAGGCTCTAAAATAACCATGGACA
ACGTGAATTGGGTAGCATCTTTTTTTTAATAGATAGTTTATTATGTATAACAATAATTTA
AAGATATTCATAGTGATAAGTAATTTTAAATGAGTTTAAAGTACTACTTTTCCTTTACCG
CCAGTTTCCTGTACTATGAAAAAGGCAAATTCCGCATTGTAGCCGCCCACACGCATTTTG
ATCATCAATTACGAAATTTGCCGCACACGTGTCACGTGATAAGCACTCTTACTATCATGT
TTTACGGAGTAGCAATGATGTTCAATTATTGCAGCTTTCTTTCGTGAAATCGTAGTATCA
TAGACCTTCCTAATGATGGAAGCGGTAAAGAAGGAAATCGTAAAAGTAAATTAACGAAGT
AGTATTAGTAAAACAGAGTTGAAAAACTGATAAATCTTCAACTCGAACTGAAAAGAAACA
CAATAGAATATTTTTTCTCAATGCTACCTTTATATCTTTTAACAAATGCGAAGGGACAAC
AAATGCAAATAGAATTGAAAAACGGTGAAATTATACAAGGGATATTGACCAACGTAGATA
ACTGGATGAACCTTACTTTATCTAATGTAACCGAATATAGTGAAGAAAGCGCAATTAATT
CAGAAGACAATGCTGAGAGCAGTAAAGCCGTAAAATTGAACGAAATTTATATTAGAGGGA
CTTTTATCAAGTTTATCAAATTGCAAGATAATATAATTGACAAGGTCAAGCAGCAAATTA
ACTCCAACAATAACTCTAATAGTAACGGCCCTGGGCATAAAAGATACTACAACAATAGGG
ATTCAAACAACAATAGAGGTAACTACAACAGAAGAAATAATAATAACGGCAACAGCAACC
GCCGTCCATACTCTCAAAACCGTCAATACAACAACAGCAACAGCAGTAACATTAACAACA
GTATCAACAGTATCAATAGCAACAACCAAAATATGAACAATGGTTTAGGTGGGTCCGTCC
AACATCATTTTAACAGCTCTTCTCCACAAAAGGTCGAATTTTAA

>YER112W, 187 aa (SEQ ID NO 148)
MLPLYLLTNAKGQQMQIELKNGEIIQGILTNVDNWMNLTLSNVTEYSEESAINSEDNAES
SKAVKLNEIYIRGTFIKFIKLQDNIIDKVKQQINSNNNSNSNGPGHKRYYNNRDSNNNRG
NYNRRNNNNGNSNRRPYSQNRQYNNSNSSNINNSINSINSNNQNMNNGLGGSVQHHFNSS
SPQKVEF

>YFR010W, 2000 bp, CDS: 501-2000 (SEQ ID NO 153)
GAAAAATTTCAACGGTGGTGTCTTAATGGTTTCCCATGATATCTCTGTTATTGACTCTGT
TTGTAAAGAGATTTGGGTTTCAGAGCAAGGTACTGTCAAGAGGTTCGAAGGTACAATTTA
CGACTATAGAGATTACATCTTGCAGTCTGCTGATGCTGCAGGTGTGGTTAAAAAGCATTG
ATTATTTAGGAAGCACCTCAGAATATATTTTCCATAGAAGCCTAAATTAAGTATGCATTC
ATAGCCCCATGATACTTTTTTTTTTGACTACTTGTATTGGAATCTAATTGACCTAACTGG
GCATTCTGGGTCATTGGTATATGTATCACTTTTTACGTAAAAAAGTAGTGGCTAATATAAA
AACATAAAATCTACAAGAAGGGTGAAGTGCTTTTCGAATTTTGCCACTGCAAGTAATTGG
TGCAATTGAAATACGAGATTTCGTTCTCTAAGAGGATATAAAAATAAGGAAATTAGCCCT
ACCTATCCTTGTGTTAAAATATGAGCGGAGAAACGTTTGAGTTCAATATTAGACATTCTG
GTAAAGTTTACCCAATAACACTTTCCACTGATGCTACTTCAGCAGATTTGAAAAGCAAAG
CAGAGGAATTGACCCAAGTCCCAAGTGCCCGCCAAAAATACATGGTTAAAGGTGGCTTGT
CTGGCGAAGAGTCCATTAAAATATATCCCTTAATCAAGCCAGGATCGACAGTAATGCTAT
TGGGGACTCCAGATGCTAACCTGATTTCTCAAACCAGCCAAAAAGAATAATTTCATTGAAG
ACCTTGCGCCTGAGCAACAAGTCCAACAATTTGCTCAATTGCCTGTTGGTTTCAAGAATA
TGGGCAACACCTGTTATCTGAATGCTACCCTACAGGCTTTATACAGAGTGAACGATTTAA
GGGATATGATTCTTAATTATAACCCTTCTCAAGGTGTGTCTAACAGTGGTGCACAAGATG
AAGAGATTCACAAACAAATCGTTATTGAAATGAAGCGTTGTTTTGAAAATTTACAGAATA
AAAGTTTCAAGAGTGTTTTGCCAATTGTGTTATTAAACACGCTAAGAAAGTGTTATCCAC
AATTTGCTGAACGTGATTCACAAGGTGGGTTCTATAAACAGCAAGACGCTGAGGAGTTGT
TTACACAACTATTCCATAGTATGAGTATTGTTTTTGGTGACAAATTTTCCGAAGATTTCA
GGATTCAATTTAAAACTACCATCAAAGACACAGCTAATGATAACGATATTACTGTTAAAG

AAAATGAAAGCGATTCTAAATTACAATGTCATATTTCTGGTACTACAAATTTCATGAGAA
ATGGGCTCCTGGAAGGTTTGAATGAGAAAATTGAAAAAAGATCAGACTTGACTGGCGCCA
ATTCCATCTATAGCGTCGAAAAGAAAATATCAAGATTACCAAAGTTTTTAACTGTTCAGT
ACGTTAGATTTTTCTGGAAAAGGTCAACCAACAAAAATCTAAAATATTGCGTAAGGTCG
TTTTCCCATTTCAATTAGATGTTGCAGACATGCTTACCCCAGAATACGCAGCAGAGAAGG
TAAAAGTTCGTGACGAACTGAGAAAAGTTGAAAAGGAGAAAAATGAAAAGGAAAGAGAGA
TCAAAAGGCGTAAATTTGACCCATCATCCAGTGAAAATGCTCATGACACCAAGAGAACAAT
ATGAGACACAAGTGGCTCTTAACGAAAGTGAAAAAGATCAATGGCTCGAAGAGTATAAGA
AACATTTCCTCCAAACTTGGAAAAAGGTGAAAACCCATCTTGTGTTTATAACTTGATCG
GTGTCATTACACATCAAGGTGCCAATTCTGAGTCTGGACACTATCAAGCTTTCATAAGGG
ACGAACTGGACGAAAATAAATGGTACAAATTTAATGATGATAAAGTTAGCGTTGTTGAAA
AGGAAAAAATTGAATCTTTAGCCGGTGGGGGCGAAAGTGATAGTGCACTGATCTTAATGT
ATAAAGGATTTGGTCTGTAA

>YFR010W, 499 aa (SEQ ID NO 154)
MSGETFEFNIRHSGKVYPITLSTDATSADLKSKAEELTQVPSARQKYMVKGGLSGEESIK
IYPLIKPGSTVMLLGTPDANLISKPAKKNNFIEDLAPEQQVQQFAQLPVGFKNMGNTCYL
NATLQALYRVNDLRDMILNYNPSQGVSNSGAQDEEIHKQIVIEMKRCFENLQNKSFKSVL
PIVLLNTLRKCYPQFAERDSQGGFYKQQDAEELFTQLFHSMSIVFGDKFSEDFRIQFKTT
IKDTANDNDITVKENESDSKLQCHISGTTNFMRNGLLEGLNEKIEKRSDLTGANSIYSVE
KKISRLPKFLTVQYVRFFWKRSTNKKSKILRKVVFPFQLDVADMLTPEYAAEKVKVRDEL
RKVEKEKNEKEREIKRRKFDPSSSENVMTPREQYETQVALNESEKDQWLEEYKKHFPPNL
EKGENPSCVYNLIGVITHQGANSESGHYQAFIRDELDENKWYKFNDDKVSVVEKEKIESL
AGGGESDSALILMYKGFGL

>YFR052W, 1325 bp, CDS: 501-1325 (SEQ ID NO 157)
CAGAGACATGTTTTAATTCAAGTGATGAGGCGGAAACGTGCAAGATCCTAAATGAAGGAT
AAAAAGAGTTCTTAAAAAGGGAAGTAAGGAATAACAGAGTAGAAAAACCGAAAAGACAAC
TTAACAAATCGGCAACACTTTTATGGGGCCCCGCTCGCCTGTGTGCAAGTAGTATTCGAC
CTGGAACACGCATTTACCACGAGAAGACAGCAATAGTCCGTACAACATTAATTAGTTTCG
ACAATTGCTCGCCTTTATAAGCCATGCTAGTGCCCAATCAAACACTTTACTTGCCCTGAA
GTTCCTTTTTCGCTAGCCTGTAACTTAAATAAGCCATCTAACCTTTTTTTTCTAAAAAT
TTTCTTTATTACCCTGTCGGCTTATTTTCTATTCTACACATTATTTGCCACCCATTGAAA
TTGTAGCTTGTATTAATAGGGAAAAGCCGGAAGTATAACCGGTGGAAAGTACTATTGAAG
TGAGATAAGAAGCCATCGTAATGCCCTCGTTAGCCGAATTGACCAAGTCGTTAAGCATAG
CCTTTGAAAACGGCGATTATGCCGCGTGTGAGAAGCTCTTGCCCCCTATCAAGATCGAAC
TTATCAAGAATAACCTTTTAATACCTGACTTATCCATTCAAAATGACATCTATTTGAATG
ATTTGATGATTACTAAAAGGATCCTGGAAGTAGGTGCCCTTGCTAGCATCCAAACTTTCA
ATTTTGACAGCTTCGAGAATTACTTCAACCAATTGAAGCCTTACTACTTTAGCAACAATC
ATAAATTATCTGAATCTGACAAGAAATCGAAGCTGATAAGTCTGTATTTGTTGAACTTAT
TGTCTCAGAATAACACAACCAAGTTTCACTCGGAATTGCAGTATCTAGATAAACATATCA
AGAACTTGGAAGACGATTCACTTTTGTCTTACCCTATCAAACTAGACAGATGGCTCATGG
AAGGGTCGTACCAGAAAGCATGGGATCTTCTGCAATCTGGGTCGCAGAATATATCAGAAT
TCGACTCTTTTACCGATATCCTAAAATCAGCTATAAGAGACGAAATTGCTAAAAATACCG
AGCTATCCTACGACTTTCTCCCTCTCTCCAACATAAAGGCTTTGCTCTTTTTCAACAACG
AAAAAGAAACTGAAAAATTTGCACTAGAGAGAAACTGGCCTATTGTCAACTCGAAAGTTT
ACTTCAATAACCAATCAAAGGAGAAAGCTGATTACGAAGATGAAATGATGCATGAAGAAG
ACCAAAAAGACAAACATTATCGAAAAAGCAATGGATTATGCCATAAGTATTGAAAATATTG
TGTAA

>YFR052W, 274 aa (SEQ ID NO 158)
MPSLAELTKSLSIAFENGDYAACEKLLPPIKIELIKNNLLIPDLSIQNDIYLNDLMITKR
ILEVGALASIQTFNFDSFENYFNQLKPYYFSNNHKLSESDKKSKLISLYLLNLLSQNNTT
KFHSELQYLDKHIKNLEDDSLLSYPIKLDRWLMEGSYQKAWDLLQSGSQNISEFDSFTDI
LKSAIRDEIAKNTELSYDFLPLSNIKALLFFNNEKETEKFALERNWPIVNSKVYFNNQSK
EKADYEDEMMHEEDQKTNIIEKAMDYAISIENIV

>YGL072C, 860 bp, CDS: 501-860 (SEQ ID NO 159)
ACTCTTTTGCTAGGGAGTTTCTGTCGCTAAGAGGTTTGTCAATGACACCGAAAAGAGGAT
AATAGGTAATACTTTTTGTAACTGTAAAGAATATTAAATCGTTTTCACGGAATTGGCCTC
TTCCCTATATTCTATCCGAGGTTGTGTACTGTAGCGGTTTATACTTCAACCTGTGAAAGT
TATGTAATATGCGAATTCTGTTTCTGCTTGATAATCTGAAGAATATAGTCTCGAGCACGC
GATGGAGCAGAAAGGGAGAAATGAATACTGATGAGCTTAACGATGAGGAGGCCGTTTCC
GTTTCTCTTGATTACCCTTTCATCCAACAGTCAATATAAGTACGCCAACTTGCGTTAAAA
CGGCCAATGTGACACCAGTTCACTCGGCAAGCCCTTCTCAGGCTCTCACTAGCTCGAATA
ACGAGAACTCTTCACGACTCATCTACTTGGCATTTTCCGGGTGCAGTTCAACCTCACTCG
CGTGCGGCGGTGTGAGGTGCATGGGTGCCGGTATTTTTTTTAGTTCGCTCTGCGCCTTAC
GCGATCAGCTTCGAGAACATACTATATTAAATGATTATATACGCTATTTAATGACCTTGC
CCTGTGTACTATTTCTTAGCTCGTTTGGGCAGGCGGTGATCGTTGTACTCTGTCGGGTCC
TGTATTTCGACTATAGCCGGTTCCGGTATTTCCTCCACAAATCTTTTCTTAGCGTTCTCG
GGCGCCGTGTCGGCCTGGGTGGAATAACTGTGGTCATTAAAGCTTGGCAGGTTATCACTC
ACTTTAGTGTTTCAGTGGCGCTGAACTTTATATCGGGGGACACCCTTGTACTTCCCTCA
CTAGTGTTATTGTCGTTTAG

>YGL072C, 119 aa (SEQ ID NO 160)
MGAGIFFSSLCALRDQLREHTILNDYIRYLMTLPCVLFLSSFGQAVIVVLCRVLYFDYSR
FRYFLHKSFLSVLGRRVGLGGITVVIKAWQVITHFSVFSGAELYIGGHPCTSLTSVIVV

>YGL080W, 893 bp, CDS: 501-893 (SEQ ID NO 161)
GAAGAAAAAGAAGAAGGGGATGATGAGGAAGGAGAAATAGAACTTGAAATTATTAGAGTA
AAAAGAATAAAGGGCAGGACGAAGATAAAGAAGACGCTTACTTGCTTCTCGAAAAACAAG
AAAATTATTACCCCTCAGCACTCCAATAGTATGTGGTACTACTAATAGTAATCTTGATT
TTTGACCGCCTACTATCGAATTAAATATAATTTTATAACCCAGTTCTATATTGCTGGGTG
GTATTATAGCTTCATGGCTAGTCAAATAAGTGGAGTTTTTTGCTCTGGACGTGGCCTGTA
AAGTTCTCTTTTGCGACGGCCCCCCGCTTTAACCGAGGCGAAATGACAAGTGCTTTCTGG
CAAAGAAGGAATAGCCACTACAACCTGCGGTCTCCACCTTTCTCCACCGATAATCTATTT
AAACACTCACTTGCCAATCAGCAAACGTCAATACATCTACATATATACGTATAGATTTTA
TTGCACTGTGATCAAAAAGAATGTCTCAACCGGTTCAACGCGCTGCAGCACGCTCATTCC
TTCAAAAATACATCAATAAAGAAACTTTGAAATATATTTTCACAACACACTTCTGGGGTC
CCGTATCAAATTTCGGTATCCCAATTGCTGCTATATATGATCTGAAAAAAGACCCTACAC
TAATCTCTGGCCCAATGACTTTTGCTTTAGTTACCTATTCAGGTGTTTTCATGAAGTATG
CTCTTTCAGTATCACCCAAAAACTACTTACTGTTTGGATGCCACCTTATTAATGAAACTG
CGCAATTAGCTCAAGGCTATAGGTTTCTCAAATACACGTATTTCACAACAGATGAGGAGA
AGAAAGCTCTAGATAAGGAATGGAAAGAGAAAGAAAAAACTGGTAAACAGTAA

>YGL080W, 130 aa (SEQ ID NO 162)
MSQPVQRAAARSFLQKYINKETLKYIPTTHFWGPVSNFGIPIAAIYDLKKDPTLISGPMT
FALVTYSGVFMKYALSVSPKNYLLFGCHLINETAQLAQGYRFLKYTYFTTDEEKKALDKE
WKEKEKTGKQ

>YGR008C, 755 bp, CDS: 501-755 (SEQ ID NO 165)
CGCAATAGTTATGAACTTAACCGAGCTCAAATAATTTAAAGATAAAAGATAAAAGATAAA
AGATAAAAGACAAAAGAAAATTCATAGCCCATGTTGAAGTATCCCAGCGGGAAATGTTGC
TATCCAACAGAAAGTACCAAGCCAGTTTCAAAAAGGTACAGAATTAAGTGATGCTATCCG
TCCCACAACTAATTTTCTCCAGCGGAGGAAATATACGCCGGAGGGGGGAGGAAAACCTCT
CAGTAAGCAATGAAGGGATAGATAATGGGGGCGCGCCTGCCTAGCTTAGGCTAAGAAACT
CCTTCGAAAACAGGGGGCTGCGAGCGCAGAAGCGAACACTTGTCATTTGTATAAAAGGAC
TATTTATAAGTTTGCTTTTTGTCACTCTCTTGGCCCTAATTACCCATACTATTGTAACAA
TTGTTGTGTAAACTCAATTATACAAATAAACGAACAATCAACAGTAACAAACCGCTCAAG
TGTACAACCAATCAGAAAAAATGACGAGAACAAACAAGTGGACCGAACGTGAAGGAAAGG
CTGATCCAAAGTACTTTTCGCACACTGGTAACTACGGTGAATCTCCAAATCACATCAAGA
AGCAAGGTTCCGGCAAGGGTAATTGGGGTAAGCCAGGCGATGAGATTGATGACTTAATTG
ATAATGGTGAAATACCCCCAGTGTTCAAGAAAGATAGAAGAGGCTCAAATTTGCAATCGC

ATGAACAAAAGTTTGAAAACGTCCAAAAGGAATGA

>YGR008C, 84 aa (SEQ ID NO 166)
MTRTNKWTEREGKADPKYFSHTGNYGESPNHIKKQGSGKGNWGKPGDEIDDLIDNGEIPP
VFKKDRRGSNLQSHEQKFENVQKE

>YGR023W, 2156 bp, CDS: 501-2156 (SEQ ID NO 167)
TTAGATCATGGCTAGGGGGATCTGGAAGTACAATGATGTGCTCTCCCCCTCTCAAACACA
ACACCAGGATGAACTAAGGGCTCATCTCGAAAGTCGAAGGTGCCTCATTCAGGTTATTAG
TGGTGCCTGTTGTGTCTTCCATGAACAAGGAGCACTTAATTACTTGTTGTTGCATGAGAT
ATCATTTTTTTTTTTCCCTCTTTCTTGGGGTCTTGACAGTCATCAAATCGAAGTTTTTAG
TTTTTCTTCTTCGGGAAGATCAATTTTAGGTAGAAAAGTGTAGATGAAAAACGAAGGATA
CTGCTATTTACTGTAAGTACTCTTCGGTCCATATTGGAAGACCAAGGCATAATAAGGATA
TATTCCGAGGAGATAATTGGGATATAATCCTCCATTGCTTCCGAAATTTCTTTAAACACT
TCTAGTTCATTTCGGGTTGGTTCGATCTTCGTTTCCACTTTTAACTTACTCCCAGTTAGT
ATAATATAAGTAGTTAAGGTATGGCAAGCTGCAATCCGACCAGGAAGAAGAGCTCTGCTT
CAAGCCTATCTATGTGGAGAACGATTCTCATGGCGTTAACAACACTACCGCTAAGTGTTC
TTTCGCAGGAGTTGGTTCCAGCTAATAGCACAACATCGAGCACAGCTCCTTCCATCACTT
CGCTTTCCGCAGTTGAGTCATTTACGTCCAGTACCGATGCAACGAGCAGCGCAAGTTTAT
CAACGCCGAGTATAGCTTCAGTATCCTTTACTTCCTTCCCACAAAGTTCTTCACTGCTTA
CTCTTTCGTCAACATTATCCTCAGAACTTTCCTCTTCGTCCATGCAAGTTTCGTCGTCTT
CAACATCGTCGTCTTCTTCGGAGGTTACGTCATCATCGTCATCATCATCAATATCTCCTT
CCTCTTCATCATCAACAATAATATCATCGTCATCATCACTGCCGACATTCACTGTGGCAT
CAACATCTTCGACAGTTGCCTCCTCCACACTTTCCACTAGCTCATCGTTGGTTATCTCTA
CGTCTTCGTCAACGTTTACGTTTAGTTCGGAAAGTTCAAGCTCTTTGATTTCCTCTTCAA
TTTCAACATCCGTTTCGACTTCTTCAGTGTACGTTCCCTCCTCTTTCAACTTCATCTCCAC
CTTCGTCCTCATCCGAATTGACATCATCCTCGTACTCATCATCCTCATCCTCATCCACCC
TCTTTTCCTACTCCTCCTCATTTTCATCATCCTCATCCTCATCATCCTCATCATCATCCT
CATCCTCATCATCATCATCATCATCATATTTCACCCTCTCCACACATTCCTCCTCTTT
CATCCATATACTCGTCTTCGTCATATCCTTCATTTTCATCTTCATCTTCCTCAAACCCTA
CCTCATCAATCACTTCTACATCCGCCTCATCTTCTATTACTCCCGCTTCCGAATTATCCA
ATTTGGCAAAAACCATAACTAGTATAATAGAAGGCCAGACCATCCTCTCTAACTACTATA
CCACAATAACGTATTCACCGACAGCATCCGCATCTTCAGGAAAAAATTCACATCACTCAG
GCTTATCAAAAAAGAATCGTAATATTATCATCGGTTGTGTGGTTGGCATAGGTGCCCCCC
TCATCCTAATTCTACTAATATTGATTTACATGTTTTGTGTTCAGCCTAAAAAAACGGATT
TCATTGACTCTGACGGTAAAATTGTCACAGCTTATCGTAGTAACATTTCACCAAAATAT
GGTATTTCTTGCTGGGTAAAAAAATTGGTGAAACAGAAAGATTCAGCTCAGATTCCCCCA
TCGGCAGCAATAATATTCAGAATTTTGGTGATATCGATCCAGAAGATATACTTAACAATG
ACAACCCCTACACCCCTAAACACACTAATGTTGAAGGCTACGACGACGACGACGACGACG
ACGCTAATGATGAAAACCTATCATCCAACTTCCATAACAGAGGCATAGATGATCAATACT
CACCTACTAAATCTGCATCATATTCAATGTCGAATAGTAATAGTCAAGATTACAACGACG
CAGATGAAGTAATGCACGATGAAAACATTCATCGTGTTTATGATGACAGCGAAGCTAGCA
TCGACGAGAACTATTACACGAAACCAAACAACGGCTTAAATATCACGAACTATTAA

>YGR023W, 551 aa (SEQ ID NO 168)
MASCNPTRKKSSASSLSMWRTILMALTTLPLSVLSQELVPANSTTSSTAPSITSLSAVES
FTSSTDATSSASLSTPSIASVSFTSFPQSSSLLTLSSTLSSELSSSSMQVSSSSTSSSSS
EVTSSSSSSSISPSSSSSTIISSSSSLPTFTVASTSSTVASSTLSTSSSLVISTSSSTFT
FSSESSSSLISSSISTSVSTSSVYVPSSSTSSPPSSSSELTSSSYSSSSSSSTLFSYSSS
FSSSSSSSSSSSSSSSSSSSSSSSYFTLSTSSSSSIYSSSSYPSFSSSSSSNPTSSITST
SASSSITPASEYSNLAKTITSIIEGQTILSNYYTTITYSPTASASSGKNSHHSGLSKKNR
NIIIGCVVGIGAPLILILLILIYMFCVQPKKTDFIDSDGKIVTAYRSNIFTKIWYFLLGK
KIGETERFSSDSPIGSNNIQNFGDIDPEDILNNDNPYTPKHTNVEGYDDDDDDDANDENL
SSNFHNRGIDDQYSPTKSASYSMSNSNSQDYNDADEVMHDENIHRVYDDSEASIDENYYT
KPNNGLNITNY

>YGR034W, 1244 bp, exon1: 501-525, intron1: 526-879, exon2: 880-1244 (SEQ ID NO 169)

TATAAAAAAAATTCTTGTAGACAATAAAATAAGAAATGCCCATTTTGTAACTTAGCGAAA
GATGCCCAGTACATCCCTTTTACACCCGTGCATTAAAGGTGTTTGGGTTTAATAGGAGCT
TTATCATATCTCTTTGATTTTTTTTCTGCTGTCCCTCGGCTTGAGGGACTCACAGAGATCT
GGAAATTTTCAGATTGTCAGTGCTTAGGATGGGTTGTCAGTAGACGGTGGCCGCCGTGGA
TGGGAAATCTCATACGTTTACACACATAGTGTTTGGAAATTAATAGTAGCAATAGCTATC
TGGCTACTGTTTTAAAGTATTAGCCCGTTCTCAGTGCTTCTTTTTTAAGGAATAACAACG
GCAAGACCAAAGATATATCAAATATGGCTAAGCAATCTCTAGGTATGTTTGGAGGATACG
AATAACGATAGAAAACATGAGTGAATTTCCGTCCACGAAAAAATGTTAACATAAAATGCA
AGAGAACAATTAATCGAATAATGTTAAATTATTGTAAAACAATGTGTATGATGAGGAGGA
ATGTACCTAAGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAACAGCTTTTGCAT
ATTCAATCCAGGCATAGGGCGACTATTTAGCACTCAACGATTTTTAAGCTTGTGTATTGC
TGACATAAATTCCGGCTTTAGAATCCAATATTGAAAAACGTGAGTACGCAGAGGAGATAG
AAGAAAAGTAGGAAGTTACCGTTTATATTGATTTGTGAAATGCATACTCCGTTGGATGTG
GGGCAACATAGATTTAAGTGTGGATGAAAATTATGTGCTCATTGTGAAAAAAAAGTTTTG
CTTTTACTAACAAATTTTTTTTATTATTTGTTTCAATAGACGTTTCCTCTGACAGAAGAA
AGGCCAGAAAGGCTTATTTCACTGCTCCATCCTCTGAACGTCGTGTTTTGTTATCTGCTC
CATTATCCAAGGAATTGAGAGCTCAATATGGTATCAAGGCTTTGCCAATCAGAAGAGACG
ATGAAGTCTTGGTTGTTCGTGGTTCCAAGAAGGGTCAAGAAGGTAAGATTTCATCTGTTT
ACAGATTGAAGTTTGCTGTTCAAGTTGACAAGGTCACCAAGGAAAAGGTCAACGGTGCTT
CCGTTCCAATTAACTTGCACCCATCCAAGCTTGTTATCACTAAGTTACACTTGGACAAGG
ACAGAAAGGCTTTGATCCAAAGAAAGGGTGGTAAATTGGAATAA

>YGR034W, 129 aa (SEQ ID NO 170)

MLNYCKTMYVSSDRRKARKAYFTAPSSERRVLLSAPLSKELRAQYGIKALPIRRDDEVLV
VRGSKKGQEGKISSVYRLKFAVQVDKVTKEKVNGASVPINLHPSKLVITKLHLDKDRKAL
IQRKGGKLE

>YGR069W, 836 bp, CDS: 501-836 (SEQ ID NO 171)

TTCGAATTATTTTGTTGAAAACAGGGCTCGAAAGTGATCTCTTGCTTAGAAATATTGCGT
TGCCGCTGGTGTCCATATCTTGGTTGCTTGTACTGCGACCGCTACTACTGTTATGTTGAT
TTTCCGCATTTTCCCCACCGACTAAAACATCCCCTTTTGAAGAAACCAATAAGTTGTCCC
AATAGCATTCGAAAATCTTACGCTTTTCCTTAACTAGACTTGCCAAACTACTGCTATTCT
TCTTATATCGGCCAACTTGCAAAAACTCCAATTTGAATCTTCCTACCAATCTCAGCGAAA
TTTTCTTCACTACGATCTCATTTTTCACTGAAATCACTAAGTTTCCTGATAAAGGTATAG
ACGACAGTTCCAACGGTGACCCTTGGATCAAAATTATGTCCTTGTACGGGGAGTTTATTC
TAATATCAAAATAACTTATTCTCTCTCTTTCCTTCTGCTCTGAATGCCCACCGCTGCTAG
ATAGCGAACTAAGTGAAAACATGGTCTTGCTTCACCCTATTCTCGCCGAGAGCTGTACAA
GATATTTTTTACTTTTGCCATCTTATACTCATCCTAATCATCTGTTTCATTTTCCTTCTA
TTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAGTTTTCGAAGAAACTGCCTTTTTA
GAATTGTAAAAGACGAAGTGAAGTATTCAGGAGTATATTATTACATACATACAAAGCAAG
ACAAAGAAACATTTTTAGATCTAACATTTTACTTCAATTGTTTTTGTATTCCTTATAATA
AGAAAGACCTGCTGTTTAATGTGGGAGTAATCCGTCCCCTACTCGATCTTCAATAA

>YGR069W, 111 aa (SEQ ID NO 172)

MVLLHPILAESCTRYFLLLPSYTHPNHLFHFPSISFFFFFFFFFSFRRNCLFRIVKDEV
KYSGVYYYIHTKQDKETFLDLTFYFNCFCIPYNKKDLLFNVGVIRPLLDLQ

>YGR070W, 3968 bp, CDS: 501-3968 (SEQ ID NO 173)

AAGAAACATTTTTAGATCTAACATTTTACTTCAATTGTTTTTGTATTCCTTATAATAAGA
AAGACCTGCTGTTTAATGTGGGAGTAATCCGTCCCCTACTCGATCTTCAATAAATTGTCA
TCTTGTATCTAAAGGAGCGCTCCAGTACTCCAATTAAGCACCACCTAGTGCGTCTAGTGT
CGATTTTTTTTTCACGCATACGTTTGTATGTTTCTTAAATTTCCCATGATTTTTTGTTGC
CAATGTCATATCTACAAACTCTATACGAAAGTAAACGCACTTCATCTTTTTTGCCCTAAA
ACGGCAATATTTAGACATATCATAAGGGGCCCAAGGGAGAATCGTTAATTTTAAACTTTT

CTTTGCTCTTGAATGAAAAAGTAAATAAATAAAACTAAATCAAAAAAAAGAACGCCACGT
TTGAATTTTAAAGCAAAAATTTTGTTGATTTAGTAATGATATAAATAAAACCAAGTCGTT
GGTAAGAATTTGGTTAGGTTATGAATAGTAATGAACTGGATCTAAGAAATAAATATTTTT
ATGAGATATTCGGTAAGAAAAGAAAATCAGATACTTCAACCCCTACTCAGTTGTTCTCCG
GCTCCAAAGTTCAGACAAACATCAATGAAATTTCTATCACTAACGATGAGGATGAAGATA
GTACTGAAGATGAAAATAAGGCTTCATTGAAGGATTATACACTAGGGCACGACACCGGTG
CACGGTATAGGATAGCACCGGACTGTTCTTCCCACCAATTAAAGGCATCTCCTGTCCTAC
ATATTTCAACAAACCTTAATTCAAGTCCACAATCCTTCACAGGCGATCAGATTTCACCTA
CTAATAAAAAAATTTCAATAAATGATTCGACCAGACAAGATAAAGGTAACAGTTGCACTA
CCACTTCATCACCTTCTCAAAAAAGATCGAATGTTTTGCTTCCTCACGTAAGAAAACATT
CATCTCCTTCACTATTATCATTTTCCAAAAACAGTGGCAGTCATATGGGGGATCCAAACC
AGCTATCTACGCCTCCAACTCCCAAAAGTGCAGGTCACACGATGGAGTTACACAGTTCAT
TCAATGGAAAACATAGTTCTTCTAGCACCTCTTCTTTATTTGCATTAGAGTCACTGAAAA
CCCAAAATAGACGCTCATCAAACTCTTCCAATCATTCTAGTCAATATCGACGCCATACTA
ATCAACACCAACGTCATCATTCAAGGTCCAAATCAAGTCCTGTCTCTCTGACGGAAATAT
CCATGATCAAAGGCACGCCTTTGGTTTATCCTGCACTTTTATCACTAATAGCAATTAAAT
TCAAACAGACCATCAAATTGAGCACGCATAAAAAGATGGGGTTACTTTACAGAGATTCCT
TTACAGGAAAACAAGCAATTGATACTTTATGCTTGATCATAGGAAGCTTAGATCGTAATT
TGGGCATGTTGATCGGAAAATCGCTGGAAGCTCAAAAATTGTTCCATGACGTACTTTATG
ACCATGGCGTAAGAGATTCTGTACTGGAGATTTACGAGTTATCTTCAGAATCAATTTTTA
TGGCACATCAGTCGCAGAGTTCTACTTCAATTGCCAACACATTTTCTTCATCATCTTCTT
CAGTTAATTCGCTCCGTACTAAAACTGAAATATATGGTGTTTTTCTCCCATTGACACATT
GTTATTCCTCTACATGCTCTCTGGAAAAACTTTGCTACTCTATTTCTTGCCCCAATCGTT
TGCAACAACAGGCTAATTTACATTTAAAATTAGGTGGTGGTCTTAAGAGAAATATTTCGT
TAGCACTCGATAAGGAGGATGATGAACGAATTTCCTGGACAAATTCCTGTACCAAAGAGCG
TATGGGAATCATTATCCAAACAACAAATCAAAAGGCAGGAGGCAATATATGAGTTGTTTA
CTACAGAAAAGAAGTTTGTAAAATCTTTGGAAATCATCCGAGATACTTTCATGAAGAAAT
TATTAGAAACGAATATTATTCCATCTGATGTAAGGATAAATTTTGTAAAGCACGTTTTCG
CACATATCAATGAAATATATTCTGTCAATAGAGAATTTTTGAAGGCTTTAGCACAAAGGC
AATCATTAAGCCCAATTTGTCCTGGAATTGCAGATATATTTTTGCAGTATCTTCCTTTCT
TTGATCCTTTTCTGTCATACATAGCATCAAGACCATACGCAAAGTATCTAATTGAAACCC
AAAGATCAGTTAATCCCAATTTTGCTCGTTTTGACGATGAAGTGTCTAATTCTTCCCTGA
GGCATGGGATCGATTCATTCCTATCTCAGGGTGTTTCAAGACCTGGTAGATATTCACTGT
TGGTAAGAGAAATAATACACTTCTCGGACCCAGTAACAGACAAAGATGATCTACAAATGC
TAATGAAAGTCCAAGATCTTTTAAAGGATCTAATGAAAAGGATTGATAGAGCAAGCGGTG
CAGCACAAGATCGTTATGACGTTAAAGTGTTAAAGCAGAAAATTCTATTCAAAAATGAAT
ACGTTAATCTGGGTTTGAATAACGAAAAAAGGAAAATCAAGCATGAAGGTTTACTCTCAA
GGAAGGACGTGAACAAAACAGATGCGTCCTTTCAGGAGACATTCAATTTTACCTACTCG
ACAATATGCTATTATTCTTGAAATCAAAAGCTGTAAACAAGTGGCACCAACACACTGTAT
TTCAGAGACCAATTCCACTCCCTTTACTGTTTATTTGTCCGGCTGAGGATATGCCACCCA
TAAAAAGATATGTGACAGAAAACCCAAATTGCTCAGCGGGTGTGCTCTTACCCCAATATC
AAACGAGCAATCCCAAGAATGCTATTGTATTCGCCTATTACGGTACGAAACAACAATATC
AAGTTACTTTGTACGCCGCGAGCCGGCCGGATTACAGACATTAATAGAAAAGGTGAAAC
AAGAGCAAAAAAGGCTCCTTGATGAAACTAAACATATTACTTTTAAGCAAATGGTAGGTC
AATTCTTTCACTCATACATAAATACTAATCGCGTCAACGATGTCCTAATCTGTCATGCTG
GTAAAATTTTATTGGTTGCAACAAATATGGGACTCTTTGTTCTTAATTATGCTACATCGA
TCAATCAAAAACCAGTGCACCTTCTGCACAAAATATCAATTTCACAGATCTCTGTATTGG
AAGAATATAAAGTTATGATTCTTCTAATTGACAAAAAACTGTACGGCTGTCCTTTAGACG
TAATCGACGATGCAGAAAATGCAGATTTTCTTTTCAGAAAAAATTCTAAAGTGTTATTTA
AATATGTTGCAATGTTCAAAGACGGTTTCTGTAATGGTAAAAGAATCATTATGATTGCAC
ATCATTTTTTGCACGCCGCACAATTATTGATTGTTAATCCTTTGATATTTGATTTTAATA
GCGGTAATTTTAAAAAAAACCTAAAGGCAGGCTTGGTAGATTTTAGCGTTGATTCTGAAC
CTCTGTCCTTTTCTTTTTTGGAGAATAAGATCTGCATTGGTTGTAAAAAAAATATCAAAA
TATTAAACGTACCGGAAGTGTGTGATAAAAATGGATTTAAAATGAGGGAGCTTTTAAATC
TACATGATAACAAAGTTTTAGCGAACATGTATAAAGAGACGTTCAAAGTAGTTTCCATGT
TTCCGATAAAAAATTCAACTTTTGCATGTTTTCCAGAACTCTGCTTTTTTCTCAATAAGC

AAGGGAAGAGGGAGGAGACAAAGGGATGTTTTCATTGGGAGGGGGAACCAGAACAGTTCG
CGTGTTCCTACCCTTATATTGTGGCAATTAATAGTAACTTTATTGAAATTAGACATATAG
AAAATGGAGAACTTGTCCGCTGTGTACTTGGAAACAAGATACGTATGTTAAAATCATATG
CCAAGAAGATCTTATATTGTTATGAGGATCCTCAAGGATTTGAAATTATCGAACTGTTAA
ATTTTTGA

>YGR070W, 1155 aa (SEQ ID NO 174)
MNSNELDLRNKYFYEIFGKKRKSDTSTPTQLFSGSKVQTNINEISITNDEDEDSTEDENK
ASLKDYTLGHDTGARYRIAPDCSSHQLKASPVLHISTNLNSSPQSFTGDQISPTNKKISI
NDSTRQDKGNSCTTTSSPSQKRSNVLLPHVRKHSSPSLLSFSKNSGSHMGDPNQLSTPPT
PKSAGHTMELHSSFNGKHSSSSTSSLFALESLKTQNRRSNSSNHSSQYRRHTNQHQRHH
SRSKSSPVSLTEISMIKGTPLVYPALLSLIAIKFKQTIKLSTHKKMGLLYRDSFTGKQAI
DTLCLIIGSLDRNLGMLIGKSLEAQKLFHDVLYDHGVRDSVLEIYELSSESIFMAHQSQS
STSIANTFSSSSSSVNSLRTKTEIYGVFVPLTHCYSSTCSLEKLCYSISCPNRLQQQANL
HLKLGGGLKRNISLALDKEDDERISWTNSVPKSVWESLSKQQIKRQEAIYELFTTEKKFV
KSLEIIRDTFMKKLLETNIIPSDVRINFVKHVFAHINEIYSVNREFLKALAQRQSLSPIC
PGIADIFLQYLPFFDPFLSYIASRPYAKYLIETQRSVNPNFARFDDEVSNSSLRHGIDSF
LSQGVSRPGRYSLLVREIIHFSDPVTDKDDLQMLMKVQDLLKDLMKRIDRASGAAQDRYD
VKVLKQKILFKNEYVNLGLNNEKRKIKHEGLLSRKDVNKTDASFSGDIQFYLLDNMLLFL
KSKAVNKWHQHTVFQRPIPLPLLFICPAEDMPPIKRYVTENPNCSAGVLLPQYQTSNPKN
AIVFAYYGTKQQYQVTLYAPQPAGLQTLIEKVKQEQKRLLDETKHITFKQMVGQFFHSYI
NTNRVNDVLICHAGKILLVATNMGLFVLNYATSINQKPVHLLHKISISQISVLEEYKVMI
LLIDKKLYGCPLDVIDDAENADFLFRKNSKVLFKYVAMFKDGFCNGKRIMIAHHFLHAA
QLLIVNPLIFDFNSGNFKKNLKAGLVDFSVDSEPLSFSFLENKICIGCKKNIKILNVPEV
CDKNGFKMRELLNLHDNKVLANMYKETFKVVSMFPIKNSTFACFPELCFFLNKQGKREET
KGCFHWEGEPEQFACSYPYIVAINSNFIEIRHIENGELVRCVLGNKIRMLKSYAKKILYC
YEDPQGFEIIELLNF

>YGR132C, 1364 bp, CDS: 501-1364 (SEQ ID NO 177)
CATACATGTATCAGACGTATAGCTCCTACGATTCTCAAGAATCCAGAAGTTTGGCATATT
ATGTATAAAGGCGATGATTATGTATATTTTATGTTGTCTCCAGTAAGTGGCAGCATAACC
CGGCCAGTCTGCGCTGCATGCTGTGAAGCAGTAATATGCGATATATACCACATATATTCC
GCTTCCGTTCAGGATTTCGAAAAGAGAAACTTCAGTGAATGACTATGACTACATAGTTGG
AGTCTTAGACCATTGCAAATGAGTTATTCAAGTATGAGAGATCAACACTGATGAGAATAA
ACTCGTCTTCATGATGATACGGGTAACGCGAATGTATCGCATCAATAAATTTCAGGGAAA
GGGAGTTTGACGATCTCATGGATGCAACGGTTGAGGTATATAATATTAAGCAGAAAGAAG
AGGAAAAAAAATAAATCGGTAAACCAACCATCAACGGTACGAAACTTACATTCAAAATCA
ATAATTTACTTTAGAAAAGAATGTCTAATTCTGCCAAACTTATCGATGTCATCACCAAGG
TGGCGTTGCCCATTGGTATAATTGCTAGCGGGATTCAGTACTCCATGTATGATGTGAAGG
GTGGTTCTCGTGGTGTTATTTTCGACAGAATCAATGGTGTAAAGCAACAGGTTGTGGGTG
AAGGCACTCATTTCTTGGTGCCTTGGCTACAGAAGGCGATCATATACGATGTGAGGACGA
AACCAAAGAGCATTGCTACCAATACTGGTACGAAGGATTTGCAAATGGTGTCATTGACCT
TGAGAGTCTTACATAGACCAGAGGTCTTACAGCTACCCGCAATATACCAAAATTTGGGTC
TCGATTACGACGAAAGAGTGTTACCATCTATCGGCAATGAGGTTTTAAAGTCTATAGTAG
CTCAATTTGATGCTGCTGAGTTAATTACTCAGAGAGAAATTATTTCTCAAAAAATCAGAA
AAGAGCTTTCTACGAGGGCCAACGAATTCGGTATTAAGTTGGAAGATGTCTCTATCACTC
ATATGACGCTTTGGTCCCGAATTCACGAAAGCAGTTGAGCAGAAGCAGATTGCACAGCAAG
ATGCCGAAAGAGCCAAATTCCTTGTCCAAAAGGCAGAGCAAGAGAGACAAGCTTCTGTTA
TCAGAGCTGAAGGTGAAGCAGAAAGTGCTGAATTCATTTCAAAAGCCTTAGCTAAAGTTG
GTGATGGTCTGTTATTGATTAGAAGATTAGAAGCTTCTAAGGACATCGCTCAAACATTAG
CAAACTCATCTAACGTTGTCTATTTACCAAGTCAACATTCTGGTGGTGGTAACAGCGAGT
CTTCGGGATCACCAAATTCCTTGCTTTTGAACATTGGCCGTTAA

>YGR132C, 287 aa (SEQ ID NO 178)
MSNSAKLIDVITKVALPIGIIASGIQYSMYDVKGGSRGVIFDRINGVKQQVVGEGTHFLV
PWLQKAIIYDVRTKPKSIATNTGTKDLQMVSLTLRVLHRPEVLQLPAIYQNLGLDYDERV

LPSIGNEVLKSIVAQFDAAELITQREIISQKIRKELSTRANEFGIKLEDVSITHMTFGPE
FTKAVEQKQIAQQDAERAKFLVEKAEQERQASVIRAEGEAESAEFISKALAKVGDGLLLI
RRLEASKDIAQTLANSSNVVYLPSQHSGGGNSESSGSPNSLLLNIGR

>YGR135W, 1277 bp, CDS: 501-1277 (SEQ ID NO 179)
TTCTGAACTGAATCTGAAATTGTTAAACCTGTTTCCCTCAAAGCCTGCAAACAAAGACGA
TAGTTCCCCTATTAACACGTTGCGTAGTTTTATCGCTGATTACTCCTTCGACACCCAGGT
GAACCCTCCCAGGAAGAAGGGTGGTGTTCTACGATGGTAAGATTTTGCCATTGCCCAAAGC
CGATAAGCCTATCCCACTTCATGAATATATAACACTCGCAGAGCTCGATGTTGGAGACAG
TGAGTGAGCAGTGAATTGCTCATGTTTTCTCTGCATCCTCATTTAATGACAATTAGCCAT
GTAATAACATCTTGAGGCAGTTAAATATTCGTTACCCTGCAGGTGGCAAAAAATTTATAG
AATAAAAGCATAAAAAGATGGATATCTATGTAATAAGGAAACATTGGCAGAGCGAAGAGA
ACAGACTGCTTTCTATAAAAAGTTTTCGATCAGTCTCTATTTTAATAATTGATTATTGGA
TATAGTTAGTAGTGTTAAACATGGGTTCCAGAAGATACGATTCCAGGACAACAATTTTCT
CCCCTGAGGGACGTCTATATCAGGTTGAATACGCGCTAGAATCCATTTCACATGCAGGTA
CCGCAATTGGGATTATGGCATCTGATGGGATTGTTCTTGCAGCAGAACGCAAAGTCACAA
GTACTTTACTAGAACAAGACACCTCTACCGAAAAACTTTATAAGTTAAACGATAAAATTG
CGGTTGCCGTTGCTGGACTGACTGCAGATGCAGAAATTCTAATAAATACGGCTAGAATTC
ACGCTCAAAATTACCTTAAAACCTATAATGAAGATATACCAGTAGAAATTTTGGTGAGAA
GGCTAAGTGATATAAAACAAGGTTACACGCAACATGGTGGTTTAAGACCATTTGGTGTGT
CCTTTATCTACGCCGGTTATGACGATAGATACGGTTACCAATTGTATACATCTAATCCAT
CGGGAAACTATACAGGGTGGAAGGCTATTAGTGTTGGCGCTAACACATCAGCAGCACAAA
CCCTACTTCAAATGGACTACAAGGATGATATGAAAGTCGATGATGCCATTGAACTGGCTT
TAAAAACGTTATCCAAAACTACCGACAGTAGCGCGCTGACTTATGACAGGTTGGAATTTG
CTACTATCAGAAAGGGTGCTAATGACGGAGAAGTGTATCAGAAGATTTTCAAGCCTCAAG
AGATAAAGGATATATTGGTAAAGACTGGTATTACCAAGAAGGATGAAGACGAAGAAGCTG
ATGAAGATATGAAATAA

>YGR135W, 258 aa (SEQ ID NO 180)
MGSRRYDSRTTIFSPEGRLYQVEYALESISHAGTAIGIMASDGIVLAAERKVTSTLLEQD
TSTEKLYKLNDKIAVAVAGLTADAEILINTARIHAQNYLKTYNEDIPVEILVRRLSDIKQ
GYTQHGGLRPFGVSFIYAGYDDRYGYQLYTSNPSGNYTGWKAISVGANTSAAQTLLQMDY
KDDMKVDDAIELALKTLSKTTDSSALTYDRLEFATIRKGANDGEVYQKIFKPQEIKDILV
KTGITKKDEDEEADEDMK

>YGR155W, 2024 bp, CDS: 501-2024 (SEQ ID NO 181)
GTGTTCTCATCCGACCCTCTGATTCATTTGGTGGCCATTACATTTTCCCTCAATGACACA
TTCCCCTATTTCATAACTGATTAAAATGGTAATGGCACGTGATAGTAGTGGCTCACAAAA
CAAAATTTTCTTTCTCAGCGCTGACAAAGCTTCATTTGCATTCTAACCTTATCACAACAA
CTTCAACTTCACCCAAGTAAGGATAATCAGCTCTGTCGTGACTGATAAATGCTATATCCG
GCATATGCAGTCCACACGGCATTACCGTTTCACTAATTTATTGCCATCTTCCTCCACAGT
TTTGCACCGAAAGGAAAAAAAGAAACCAACACCGAAAATTTTTTTTCTCCTAAAGGTTAAA
GTAAACGCAAGGCACTTCACCAGGCTTGTATATATAAATGTCGTGATGCTTCTATGCCAA
AGTAAAAGGCAACACTTGAAGATTTCGTTGTAGGCCACTTGCTCAAAGGACATCTAGATA
AATACGACGTAAGAATAAAAATGACTAAATCTGAGCAGCAAGCCGATTCAAGACATAACG
TTATCGACTTAGTTGGTAACACCCCATTGATCGCACTGAAAAAATTGCCTAAGGCTTTGG
GTATCAAACCACAAATTTATGCTAAGCTGGAACTATACAATCCAGGTGGTTCCATCAAAG
ACAGAATTGCCAAGTCTATGGTGGAAGAAGCTGAAGCTTCCGGTAGAATTCATCCTTCCA
GATCTACTCTGATCGAACCTACTTCTGGTAACACCGGTATCGGTCTAGCTTTAATCGGCG
CCATCAAAGGTTACAGAACTATCATCACCTTGCCGGAAAAAATGTCTAACGAGAAAGTTT
CTGTCCTAAAGGCTCTGGGTGCTGAAATCATCAGAACTCCAACTGCTGCTGCCTGGGATT
CTCCAGAATCACATATTGGTGTTGCTAAGAAGTTGGAAAAAGAGATTCCTGGTGCTGTTA
TACTTGACCAATATAACAATATGATGAACCCAGAAGCTCATTACTTTGGTACTGGTCGCG
AAATCCAAAGACAGCTAGAAGACTTGAATTTATTTGATAATCTACGCGCTGTTGTTGCTG
GTGCTGGTACTGGTGGGACTATTAGCGGTATTTCCAAGTACTTGAAAGAACAGAATGATA
AGATCCAAATCGTTGGTGCTGACCCATTCGGTTCAATTTTAGCCCAACCTGAAAACTTGA

ATAAGACTGATATCACTGACTACAAAGTTGAGGGTATTGGTTATGATTTTGTTCCTCAGG
TTTTGGACAGAAAATTAATTGATGTTTGGTATAAGACAGACGACAAGCCTTCTTTCAAAT
ACGCCAGACAATTGATTTCTAACGAAGGTGTCTTGGTGGGTGGTTCTTCCGGTTCTGCCT
TCACTGCGGTTGTGAAATACTGTGAAGACCACCCTGAACTGACTGAAGATGATGTCATTG
TTGCCATATTCCCAGATTCCATCAGGTCGTACCTAACCAAATTCGTCGATGACGAATGGT
TGAAAAAGAACAATTTGTGGGATGATGACGTGTTGGCCCGTTTTGACTCTTCAAAGCTGG
AGGCTTCGACGACAAAATACGCTGATGTGTTTGGTAACGCTACTGTAAAGGATCTTCACT
TGAAACCGGTGTTTCCGTTAAGGAAACCGCTAAGGTCACTGATGTTATCAAGATATTAA
AAGACAATGGCTTTGACCAATTGCCTGTGTTGACTGAAGACGGCAAGTTGTCTGGTTTAG
TTACTCTCTCTGAGCTTCTAAGAAAACTATCAATCAATAATTCAAACAACGACAACACTA
TAAAGGGTAAATACTTGGACTTCAAGAAATTAAACAATTTCAATGATGTTTCCTCTTACA
ACGAAAATAAATCCGGTAAGAAGAAGTTTATTAAATTCGATGAAAACTCAAAGCTATCTG
ACTTGAATCGTTTCTTTGAAAAAAACTCATCTGCCGTTATCACTGATGGCTTGAAACCAA
TCCATATCGTTACTAAGATGGATTTACTGAGCTACTTAGCATAA

>YGR155W, 507 aa (SEQ ID NO 182)
MTKSEQQADSRHNVIDLVGNTPLIALKKLPKALGIKPQIYAKLELYNPGGSIKDRIAKSM
VEEAEASGRIHPSRSTLIEPTSGNTGIGLALIGAIKGYRTIITLPEKMSNEKVSVLKALG
AEIIRTPTAAAWDSPESHIGVAKKLEKEIPGAVILDQYNNMMNPEAHYFGTGREIQRQLE
DLNLFDNLRAVVAGAGTGGTISGISKYLKEQNDKIQIVGADPFGSILAQPENLNKTDITD
YKVEGIGYDFVPQVLDRKLIDVWYKTDDKPSFKYARQLISNEGVLVGGSSGSAFTAVVKY
CEDHPELTEDDVIVAIFPDSIRSYLTKFVDDEWLKKNNLWDDDVLARFDSSKLEASTTKY
ADVFGNATVKDLHLKPVVSVKETAKVTDVIKILKDNGFDQLPVLTEDGKLSGLVTLSELL
RKLSINNSNNDNTIKGKYLDFKKLNNFNDVSSYNENKSGKKKFIKFDENSKLSDLNRFFE
KNSSAVITDGLKPIHIVTKMDLLSYLA

>YHR095W, 935 bp, CDS: 501-935 (SEQ ID NO 207)
GACACCTTTTCCGGTGTTTGGAGGGGCAACGGCGGGTTGCACTTGACTTTCACTTAAGTT
GTCGTGAAAACTTTCATTTTTACCTTCTGGAGTATTCATGGCCTTTGAACGACCAGATTC
CAATTCATATGAGTTGGATGAATTGGATTTCTGAGGAGATATTAGATCGGGAGTTGAATT
CATGATTTTATACGTATATCAACTAGTTGACGATTATGATATCCTTTATAGATTTTAAGGTGG
GGAAAGAACATGAGACCCCAGATGGAATTGATTATGGGGACATTGTTGCCTTTATATATA
ATTTCAATATACTAATTCAAATGATTAAAAACGTGAGGGGGACACGCAACTTCGGGTGTT
AAGAAATATTTTGCTACATTAGATAATGGTGGAGTTTCCTGGCTTGTCGGATAAAAGCCA
TCAAATGTCGCAGCAGCTCATGTTTACGTTTGCTGTCTTCTGCCCACGTCATATGAGTGG
TATTCTTCTATCAGCACTTGATGAATATTCTTTTTCTCATATATCTGAAAGACAAAAGAT
CGGCACGGCAATGCCCTGCAGCATTTCTTCCTAGTTTTTCCGAATTTCCATTACGTATTG
GATCTTGTGCGCATATTTGTCAGTCCTTCACGGAAAAAAAAAAAGAGCACTGGGTCACTT
CGGAAAAACTTTGACTCAATGCAACAGTGTCATAATCCTTTGCGCTGTCTCTTTGAAGA
AAAATCAGGAGTGCAAGATATCGATTAATTCCTTGGAAGTTATGATGGTTAGTCTTAGTT
TAACTCTCTTGAAGAAGGGTTTTTTCAGTTGGTCAACACTCTTTAGAGGTAAAAAAAAA
AAAAAAAAAAAAAAAAGAGAATTCTTCATGTAATTTACCATGATTCTACGTTTTTGCAAG
CAAAAATGAAGATAATCCGAGCGCATGCGAAGTAG

>YHR095W, 144 aa (SEQ ID NO 208)
MNILFLIYLKDKRSARQCPAAFLPSFSEPPLRIGSCAHICQSFTEKKKEHWVTSEKLLTQ
CNSVIILCAVSLKKNQECKISINSLEVMMVSLSLTLLKKGFFSWSTLFRGKKKKKKKKR
ILHVIYHDSTFLQAKMKIIRAHAK

>YHR138C, 845 bp, CDS: 501-845 (SEQ ID NO 209)
CTACGAAAATAAGCAAAAAATAAATAAAATAAAAACAAAAACAAAAACAAAAACAAAAAC
AAAAACAAAAACAAAAACACATATTGTTATGATGACTGGACGAAAGAAAGATCGTCGTTA
CTTTCCTAATTGTTTGTCTTCAGTACAGTTATTATCAGTGTTCTCTTTCTTTTTTATTGT
ACTATGTGATGTTACTGATACATCACGCGCTTCCTTTATGTTTTCTTTTTTTATGTTCGT
TACAGGATTTATAGTTTTTACAGTATATTGACTTCAATAATTTCTAATATTCAGTTCCTA
TTAAATTTGATTATTCCGATTAGATCGGTCGGCGCTACCAAAAAGAGGCGAAGAAAAGAG

GAAAACGCAAGTGGATAAAGGGGTGGGGGGCAAAAGTATTTAAGAAAAAGCGATGCGATG
GAGAGAACAAATGGATAAGTTGCGTTTCCTCGTTATATTACAACATTTAAATCTATTGTG
TAACAGACTATAGCATATATATGAAGGCCAGTTACTTAGTTTTGATTTTCATTAGCATAT
TCTCCATGGCACAGGCATCTTCCTTATCATCATACATCGTAACTTTCCCCAAGACGGATA
ATATGGCTACGGACCAGAATAGCATTATTGAAGATGTCAAAAAATATGTGGTGGACATAG
GGGGTAAAATAACACACGAATATAGCTTGATAAAGGGCTTTACAGTGGACTTACCTGATA
GCGACCAAATTTTGGACGGTCTGAAAGAACGTTTGAGCTATATTGAAAGCGAGTACGGTG
CTAAATGCAATTTGGAAAAGGATTCAGAAGTTCATGCTCTAAACCGTGACCATTTAGTTG
CTTAG

>YHR138C, 114 aa (SEQ ID NO 210)
MKASYLVLIFISIFSMAQASSLSSYIVTFPKTDNMATDQNSIIEDVKKYVVDIGGKITHE
YSLIKGFTVDLPDSDQILDGLKERLSYIESEYGAKCNLEKDSEVHALNRDHLVA

>YHR179W, 1703 bp, CDS: 501-1703 (SEQ ID NO 215)
ATATCTTACGTAATGAACTTCCGTAATGAACTTCCGTAATTCAAGATCTCTTAGCATCTC
TTGTTCAATCTTCAGACTCTACTAAGTGTTCTTACCAACCATTGGATGCTCATTACAAAT
GAATGAATATATTGCACGGAACGGAAGCGGCATGCTTTTTCCGTCTCGTGTGCTTAGTAA
AGCAAAACGGAGTAGAATCGGTAAGAACTTCCTTTTTGGGTTGGAAAATCATTGCCATTG
TTTGGACACCTTTCTTTTTCCGTATTGTTCGAGCACCGCGTTTCTTTTTGGGTACTTGAT
GAGGTAGCAGATTCCTGGAACGTGCTTTCTCTCGAGGTAACCTGCCTTGTTCCTCCTGGT
GACTTTCTAAAATATAAAAGGAAAAGCATATCTCTAGTTTCGAGTTTTTTCTTCATACTT
TATTTCCTTATGTTAAACGGTCCAGATATAGAATAAATCATCATATTAAGCTAAATATAG
ACGATAATATAGTATCGATAATGCCATTTGTTAAGGACTTTAAGCCACAAGCTTTGGGTG
ACACCAACTTATTCAAACCAATCAAAATTGGTAACAATGAACTTCTACACCGTGCTGTCA
TTCCTCCATTGACTAGAATGAGAGCCCAACATCCAGGTAATATTCCAAACAGAGACTGGG
CCGTTGAATACTACGCTCAACGTGCTCAAAGACCAGGAACCTTGATTATCACTGAAGGTA
CCTTTCCCTCTCCACAATCTGGGGGTTACGACAATGCTCCAGGTATCTGGTCCGAAGAAC
AAATTAAAGAATGGACCAAGATTTTCAAGGCTATTCATGAGAATAAATCGTTCGCATGGG
TCCAATTATGGGTTCTAGGTTGGGCTGCTTTCCCAGACACCCTTGCTAGGGATGGTTTGC
GTTACGACTCCGCTTCTGACAACGTGTATATGAATGCAGAACAAGAAGAAAGGCTAAGA
AGGCTAACAACCCACAACACAGTATAACAAAGGATGAAATTAAGCAATACGTCAAAGAAT
ACGTCCAAGCTGCCAAAAACTCCATTGCTGCTGGTGCCGATGGTGTTGAAATCCACAGCG
CTAACGGTTACTTGTTGAACCAGTTCTTGGACCCACACTCCAATAACAGAACCGATGAGT
ATGGTGGATCCATCGAAAACAGAGCCCGTTTCACCTTGGAAGTGGTTGATGCAGTTGTCG
ATGCTATTGGCCCTGAAAAAGTCGGTTTGAGATTGTCTCCATATGGTGTCTTCAACAGTA
TGTCTGGTGGTGCTGAAACCGGTATTGTTGCTCAATATGCTTATGTCTTAGGTGAACTAG
AAAGAAGAGCTAAAGCTGGCAAGCGTTTGGCTTTCGTCCATCTAGTTGAACCTCGTGTCA
CCAACCCATTTTTAACTGAAGGTGAAGGTGAATACAATGGAGGTAGCAACAAATTTGCTT
ATTCTATCTGGAAGGGCCCAATTATTAGAGCTGGTAACTTTGCTCTGCACCCAGAAGTTG
TCAGAGAAGAGGTGAAGGATCCTAGAACATTGATCGGTTACGGTAGATTTTTTATCTCTA
ATCCAGATTTGGTTGATCGTTTGGAAAAAGGGTTACCATTAAACAAATATGACAGAGACA
CTTTCTACAAAATGTCAGCTGAGGGATACATTGACTACCCTACGTACGAAGAAGCTCTAA
AACTCGGTTGGGACAAAAATTAA

>YHR179W, 400 aa (SEQ ID NO 216)
MPFVKDFKPQALGDTNLFKPIKIGNNELLHRAVIPPLTRMRAQHPGNIPNRDWAVEYYAQ
RAQRPGTLIITEGTFPSPQSGGYDNAPGIWSEEQIKEWTKIFKAIHENKSFAWVQLWVLG
WAAFPDTLARDGLRYDSASDNVYMNAEQEEKAKKANNPQHSITKDEIKQYVKEYVQAAKN
SIAAGADGVEIHSANGYLLNQFLDPHSNNRTDEYGGSIENRARFTLEVVDAVVDAIGPEK
VGLRLSPYGVFNSMSGGAETGIVAQYAYVLGELERRAKAGKRLAFVHLVEPRVTNPFLTE
GEGEYNGGSNKFAYSIWKGPIIRAGNFALHPEVVREEVKDPRTLIGYGRFFISNPDLVDR
LEKGLPLNKYDRDTFYKMSAEGYIDYPTYEEALKLGWDKN

>YIL074C, 1910 bp, CDS: 501-1910 (SEQ ID NO 219)
TGGGAGTCTTTAGCAAGTTCGGCAAATATCGATATCAATAGTATTGCTAAATAAACCTTT

TTTATTCCATTTACTGTCGTTTATACTGGCTGACCCTTAATTCCCTAGCAATCTTTGCCT
GCACCCGTACCAGGAAGCGTGATAGAATCGGTAGCTACAAAATTTTTAGCATAGTTAATA
AGTGCTATTGTTTTTCATAATGTCACGTGCACTATCAATAATATTACACTCTTGTTCTTG
CCAAATATACACAAAATGCCACATTTTTTTCTTTACACCGAAGAATTTGGCCGTCAGCCG
GACAGCCGTCAGATTAATTGTGGGCTAGATTCTTCACGCTGGAAACGAGTCACCGTTATG
AAAACTAATGGAATCTCCCAGGTTTAATACATAAGAAGGTTACGAGCTACTACATTAAAA
AATACTTTGTCTGTTTTAGCTGTAGATTATTGTAACATTAAAAAGTAACAAACACTGATT
TCGGGTATTTCCTCCCTAACATGTCTTATTCAGCTGCCGATAATTTACAAGATTCATTCC
AACGTGCCATGAACTTTTCTGGCTCTCCTGGTGCAGTCTCAACCTCACCAACTCAGTCAT
TTATGAACACACTACCTCGTCGTGTAAGCATTACAAAGCAACCAAAGGCTTTAAAACCTT
TTTCTACTGGTGACATGAATATTCTACTGTTCGAAAATGTCAATGCAACTGCAATCAAAA
TCTTCAAGGATCAGGGTTACCAAGTAGAGTTCCACAAGTCTTCTCTACCTGAGGATGAAT
TGATTGAAAAAATCAAAGACGTACACGCTATCGGTATAAGATCCAAAACTAGATTGACTG
AAAAAATACTACAGCATGCCAGGAATCTAGTTTGTATTGGTTGTTTTTGCATAGGTACCA
ATCAAGTAGACCTAAAATATGCCGCTAGTAAAGGTATTGCTGTTTTCAATTCGCCATTCT
CCAATTCAAGATCCGTAGCAGAATTGGTAATTGGTGAGATCATTAGTTTAGCAAGACAAT
TAGGTGATAGATCCATTGAACTGCATACAGGTACATGGAATAAAGTCGCTGCTAGGTGTT
GGGAAGTAAGAGGAAAAACTCTCGGTATTATTGGGTATGGTCACATTGGTTCGCAATTAT
CAGTTCTTGCAGAAGCTATGGGCCTGCATGTGCTATACTATGATATCGTGACAATTATGG
CCTTAGGTACTGCCAGACAAGTTTCTACATTAGATGAATTGTTGAATAAATCTGATTTTG
TAACACTACATGTACCAGCTACTCCAGAAACTGAAAAAATGTTATCTGCTCCACAATTCG
CTGCTATGAAGGACGGGGCTTATGTTATTAATGCCTCAAGAGGTACTGTCGTGGACATTC
CATCTCTGATCCAAGCCGTCAAGGCCAACAAAATTGCAGGTGCTGCTTTAGATGTTTATC
CACATGAACCAGCTAAGAACGGTGAAGGTTCATTTAACGATGAACTTAACAGCTGGACTT
CTGAGTTGGTTTCATTACCAAATATAATCCTGACACCACATATTGGTGGCTCTACAGAAG
AAGCTCAAAGTTCAATCGGTATTGAGGTGGCTACTGCATTGTCCAAATACATCAATGAAG
GTAACTCTGTCGGTTCTGTGAACTTCCCAGAAGTCAGTTTGAAGTCTTTGGACTACGATC
AAGAGAACACAGTACGTGTCTTGTATATTCATCGTAACGTTCCTGGTGTTTTGAAGACCG
TTAATGATATCTTATCCGATCATAATATCGAGAAACAGTTTTCTGATTCTCACGGCGAGA
TCGCTTATCTAATGGCAGACATCTCTTCTGTTAATCAAAGTGAAATCAAGGATATATATG
AAAAGTTGAACCAAACTTCTGCCAAAGTTTCCATCAGGTTATTATACTAA

>YIL074C, 469 aa (SEQ ID NO 220)
MSYSAADNLQDSFQRAMNFSGSPGAVSTSPTQSFMNTLPRRVSITKQPKALKPFSTGDMN
ILLLENVNATAIKIFKDQGYQVEFHKSSLPEDELIEKIKDVHAIGIRSKTRLTEKILQHA
RNLVCIGCFCIGTNQVDLKYAASKGIAVFNSPFSNSRSVAELVIGEIISLARQLGDRSIE
LHTGTWNKVAARCWEVRGKTLGIIGYGHIGSQLSVLAEAMGLHVLYYDIVTIMALGTARQ
VSTLDELLNKSDFVTLHVPATPETEKMLSAPQFAAMKDGAYVINASRGTVVDIPSLIQAV
KANKIAGAALDVYPHEPAKNGEGSFNDELNSWTSELVSLPNIILTPHIGGSTEEAQSSIG
IEVATALSKYINEGNSVGSVNFPEVSLKSLDYDQENTVRVLYIHRNVPGVLKTVNDILSD
HNIEKQFSDSHGEIAYLMADISSVNQSEIKDIYEKLNQTSAKVSIRLLY

>YIR037W, 992 bp, CDS: 501-992 (SEQ ID NO 221)
GTTTTCCATGCTTTTGCCGGATTTCCTCCACCAACGCTTCCATTCGAGACCTGTCCGTGA
TGTCGAGGACACGATAGACAAATTTGTCTGCACCGTATTCTCTTTGCAAAGACTGCAGAC
CAGCTTCCGTTCTTGCTACGCCGTAGACGATGCATTCATCGTCCTCTTCGATAACAGTTT
TCACCAATTGCAGGCCAATCCCACGGGAGGCACCTGTAATCAAAATAACCTTGCCCATAT
CCCTTCTTTGACAGATTATAAGTTCTTTCTCTTGTTGCTGTTCGCGACAGCCCTTATTTC
CTGTATTCCTTCTTCTTTTTCTGCATTATCGTTTTTAGCCACTTTACGAAAAAGGTCAAA
AAGTGAAAAAAAGAGGGAAAAAACCATGAGGAACAGTATGCTCCCTTAATATCGGAAAAG
CAATAGTAATAAAAACAGCATCAGAGCTTTCCACGTCTCTCTCTTCCAAGCTGTCATCTC
GTAAAGTATTCAAGTTTATCATGTCAGAATTCTATAAGCTAGCACCTGTTGACAAGAAAG
GCCAACCATTCCCCTTCGACCAATTAAAGGGAAAAGTGGTGCTTATCGTTAATGTTGCCT
CCAAATGTGGATTCACTCCTCAATACAAAGAACTAGAGGCCTTGTACAAACGTTATAAGG
ACGAAGGATTTACCATCATCGGGTTCCCATGCAACCAGTTTGGCCACCAAGAACCTGGCT
CTGATGAAGAAATTGCCCAGTTCTGCCAACTGAACTATGGCGTGACTTTCCCCATTATGA

AAAAAATTGACGTTAATGGTGGCAATGAGGACCCTGTTTACAAGTTTTTGAAGAGCCAAA
AATCCGGTATGTTGGGCTTGAGAGGTATCAAATGGAATTTTGAAAAATTCTTAGTCGATA
AAAAGGGTAAAGTGTACGAAAGATACTCTTCACTAACCAAACCTTCTTCGTTGTCCGAAA
CCATCGAAGAACTTTTGAAAGAGGTGGAATAG

>YIR037W, 163 aa (SEQ ID NO 222)
MSEFYKLAPVDKKGQPFPFDQLKGKVVLIVNVASKCGFTPQYKELEALYKRYKDEGFTII
GFPCNQFGHQEPGSDEEIAQFCQLNYGVTFPIMKKIDVNGGNEDPVYKFLKSQKSGMLGL
RGIKWNFEKFLVDKKGKVYERYSSLTKPSSLSETIEELLKEVE

>YJL161W, 1043 bp, CDS: 501-1043 (SEQ ID NO 229)
TCATAAAGTCTGGCGGCGTATTCCTTGCACAATTTTCATATCTTCCCATATGAATACCTG
TTAGTCCGTATCACCAAGTGTAAACTGTTCTTTACAATGAGAACATCTAGAGTCTTTCTG
ATATGCGTAACTTCTGCCTCATTAATTTAAAAATTTCTTCATAGTAAATAGCTTATTTGC
TTGGAGCAGATGATCGACATGTATTTTTAGGAACATAAACTGCCTAAATATAATAGATCA
GCCTAAAAATAAGAATGCCAATCAACAAAGTTGTATTTCCTATCTTCCGATATTCGCAGT
CCACCATTCAGACCTCTGGTGAGATAGTTTGCCTGCTTTTGCTCCCTTCCAAAGTGCTGA
TAAAAACCTCCGTGATTTTTTGAATACTCCCCTGAATGTCTATTTTAAGTATATTATAAA
ATTAGTTTAAGTTGGTGCGGATAACGAAAACTTGATGCAAGGTAAATAAATCAAGTATAT
CATAGAGTTCTTTCATTCATATGCTATACACAAGGTTGTTACGTCACAACTCACAATTCA
CCAAGTTTTCAGGCACATCGCCCAATCTTGGCTCAAAACCTTTATTTTTCGAAGGGTAATT
TGTACACTAGTCTTTTAGTGACAACACTGTATGGGACAGGTCTGGCATGCCTATATCTAG
AATCAAATAGCTTGAATAAGTCCAAAGAGCAAGAAGATCCCCATGCCATCGCAGAAGACG
ACATTGTAAATATAGTCCATGACGCTCCCAATAGAATATTCAAGCCAGCACTTGATACCT
ATCAAGAGAAAGAGCTTGACTTACAAAAGAGTGACCTCCATAAAGTACTTCATTCTTTGA
CGTACAGTGATGTCTCTCAATTTTCGATTGTTTGGGGGTTTCTCATTCAACTTTCGAGCC
TAATAGGCAATTCCACCTTAGGCAAAAAATCCATTCTTTATAAGGGAAGTGTCGTTAGTG
TTTTAGGGTTCCCACCGTTGATTTATATGGCACTTAAACTTAGGATGAAACAGCTGGAAA
AAGCTGGAGTGCGCTTTGAGTAA

>YJL161W, 180 aa (SEQ ID NO 230)
MLYTRLLRHNSQFTKFSGTSPNLGSKPLFSKGNLYTSLLVTTLYGTGLACLYLESNSLNK
SKEQEDPHAIAEDDIVNIVHDAPNRIFKPALDTYQEKELDLQKSDLHKVLHSLTYSDVSQ
FSIVWGFLIQLSSLIGNSTLGKKSILYKGSVVSVLGFPPLIYMALKLRMKQLEKAGVRFE

>YJR096W, 1349 bp, CDS: 501-1349 (SEQ ID NO 233)
GTATATTCAAGAAGAATGACACACCAAAGCCAAAGCCATTAAAGTAGATGATGAACAATG
GGACTACAAAATGAAATAAAGAAAAAATAGAAATAGGCTAGAAGATCAATTATTAATCGC
CCTATTCTTCCTTATTACCTACACAAAATAAAGCAGCAACATAAGAAACAAAAACAAAAT
GAAAACAAACCAAATAAATCTATGTAAGCATACTCATTTCAATTTGATATTCATTACTTG
ACTTTTTTGTCCTTATTTGAGGCTCCATAAGCGCGCCATTTTTCCCTACTCCCTTTTTTC
GTAAATAGTAATAATGTGCTGAAAAGAACAATGAAGTAGTTATCATACATATTCCGTCGT
GTCGATATGAGGGGAGGTGTCTCTTTCTTTCATCCCTGTCGCAACCTCCAATATATAAG
AGCATAAGCAACTGATCTTACTTTAGTAATTAACTTAGCATACCTAGCCCGAAGGAAGAA
AAAAAATTCACCTCAACAACATGGTTCCTAAGTTTTACAAACTTTCAAACGGCTTCAAAA
TCCCAAGCATTGCTTTGGGAACCTACGATATTCCAAGATCGCAAACAGCCGAAATTGTGT
ATGAAGGTGTCAAGTGCGGCTACCGTCATTTCGATACTGCTGTTCTTTATGGTAATGAGA
AGGAAGTTGGCGATGGTATCATTAAATGGTTGAACGAAGATCCAGGGAACCATAAACGTG
AGGAAATCTTCTACACTACTAAATTATGGAATTCGCAAAACGGATATAAAAGAGCTAAAG
CTGCCATTCGGCAATGTTTGAATGAAGTCTCGGGCTTGCAATACATCGATCTTCTTTTGA
TTCATTCGCCACTGGAAGGTTCTAAATTAAGGTTGGAAACTTGGCGCGCCATGCAAGAAG
CGGTTGATGAAGGATTGGTTAAGTCTATAGGGGTTTCCAACTATGGGAAAAAGCACATTG
ATGAACTTTTGAACTGGCCAGAACTGAAGCACAAGCCAGTGGTCAACCAAATCGAGATAT
CACCTTGGATTATGAGACAAGAATTAGCAGATTACTGTAAATCTAAAGGTCTCGTCGTCG
AAGCCTTTGCCCCATTGTGTCACGGCTACAAAATGACTAATCCAGATTTATTAAAAGTTT
GCAAAGAGGTGGACCGTAATCCAGGTCAAGTTTTGATTCGTTGGTCTTTACAACACGGTT

ATTTACCACTACCGAAGACTAAAACTGTGAAGAGGTTAGAAGGTAACCTTGCAGCCTACA
ACTTTGAACTGTCAGACGAACAGATGAAATTTCTTGATCATCCTGATGCTTATGAGCCTA
CCGATTGGGAATGCACAGACGCGCCATAA

>YJR096W, 282 aa (SEQ ID NO 234)
MVPKFYKLSNGFKIPSIALGTYDIPRSQTAEIVYEGVKCGYRHFDTAVLYGNEKEVGDGI
IKWLNEDPGNHKREEIFYTTKLWNSQNGYKRAKAAIRQCLNEVSGLQYIDLLLIHSPLEG
SKLRLETWRAMQEAVDEGLVKSIGVSNYGKKHIDELLNWPELKHKPVVNQIEISPWIMRQ
ELADYCKSKGLVVEAFAPLCHGYKMTNPDLLKVCKEVDRNPGQVLIRWSLQHGYLPLPKT
KTVKRLEGNLAAYNFELSDEQMKFLDHPDAYEPTDWECTDAP

>YKL065C, 1121 bp, CDS: 501-1121 (SEQ ID NO 241)
CTGGGCTAGGTTTCACATATCAAAAAGAAGTTATGGCTTATGTGCTCTTTCTAAGTTTGA
CTTTATGCCAAAAATTTCTCCGTAGATCGCCGCCCGTTGAAGCAGCAGAATATTTTAAGT
GCGCCATAAAAACCTAGATAGAAAAGAAGGGAGAGAACATAAACGCAGAACACCACTACT
TTTAAGGCGTACGCAAACTGTTGGGCTTATCTATATTGTACTATCTACCTACTTGCAACG
TCTTTTACCTCCTCGATACGTACTGCTTATGCCCTGAACAATTTACATGTAACCCGCAGC
TGCATGCTATATCACAGGATACGTTAACATAAAGGGGGCGCTACTAAACCCTCTGGCGCA
GTGCAAAAATAGAAATATATGCCAAGTGGGACCTTGTATAGTTTCTGGTTTAAAGCTATT
CGTTCATTGCAACGCTCCTTTCTGCTATCCTTTCGCAAAGTGGCAAGTACTGAAAACCGA
GAAGAATAAATAATATTGCGATGAGTTTATACTTTACGACATTATTTTTATTGCTCACTG
TTGAGGTGGTAATGCTCTTCATCTTCGTTTTGCCTTTGCCATTCCGGATCCGTAGGGGTA
TTTTTAGCACCTATAACCAATTGACAGCGAAGCAGCAAATAAAAACTATAATCTTTATAA
CGGGTTGTCTTGTTGGCCTGTTGTTTATTGATTCATGGAAAAGGTCTCAAATTCGTGTTT
CATTATACCACAACGACAACAGTGGCTCAATCGGGTCATCTGCTGTAACTCCAATACAGG
CACTAGCATCAAGAGCGTACAATCAAAGAAATATGTATATTTCCGGGTTCATATTGTACT
TTTCTATCTGTATCCCAACTGTCATGTCTATTGTCAAGAGACTGGTGAAATACTCAAGGCT
TAATCAACGAACAAGAAAAGCAAAAATTGAACAAACCTTCCTCAAACAGCAAGAAAGACT
CAAATGAAGCTGATTCCACCAAACTTCAAGAGGAACTAAGGAAAAGCAAATTTCTCTGG
AGGGCCTACAAAAGCAAGTCAAAAACCTGGAGAAATATTTTGATGAGAAGAATCAACCTG
GAAATGTAGCAGCTGCTGAAGCTTCCAAGAAAGGAAACTAA

>YKL065C, 206 aa (SEQ ID NO 242)
MSLYFTTLFLLLTVEVVMLFIFVLPLPFRIRRGIFSTYNQLTAKQQIKTIIFITGCLVGL
LFIDSWKRSQIRVSLYHNDNSGSIGSSAVTPIQALASRAYNQRNMYISGFILYFSICIPT
VMSIVKRLVKYQGLINEQEKQKLNKPSSNSKKDSNEADSTKLQEELRKKQISLEGLQKQV
KNLEKYFDEKNQPGNVAAAEASKKGN

>YKL196C, 1103 bp, CDS: 501-1103 (SEQ ID NO 253)
AAAGAGCTTCCTATTAGGAGCAATAAAATATAAAGCACCAGCCATAGAAAGAATCCCCA
TTATAAAGCCCGCTGTTTTTTCCTGATTGGAGTTCCTACCGAACTGAGGGGAGGACGCCA
TGAGACGTCTTGTTTGGTGTCGGCATAACCCCCTTGCCACTTGAATTGACGGCCTGTTTC
TGCACGCATTCCTGACGACTAAGTTGCGAAGCATTTTACTGATAATATACACTCTTTGGA
TCGAGCCTACTTCCAGTTGGTAATTGGTGTTCCACAATTTCAGCATTATATGTTTTTAAA
CCAAAATTCGGCTCCTTTTCCCTTTTTTTCTTATTGGGTGGCGTGCCGTACAGAACGATT
GGCTTGGTGTGAAATCAAGAGCAAGCACAATAGATATCAACATGAACAATATACAAAAGT
CTCTGGCACAGTTTGACTGCGTTAGACCAGGCTAGGGCATTTCTGAAGCTTTACGTATCA
CTAGAGAAGTTATTTTGGCAATGAGAATCTACTACATCGGTGTATTTCGCTCTGGAGGAG
AAAAGGCTCTAGAGTTGAGTGAAGTTAAAGACTTGTCACAATTTGGTTTCTTTGAAAGGT
CTAGTGTTGGCCAGTTTATGACTTTTTTTGCTGAAACGGTCGCTTCTAGAACTGGTGCAG
GACAAAGACAAAGTATAGAAGAAGGCAACTATATTGGCCACGTTTATGCCAGGAGTGAGG
GCATATGTGGTGTTTTGATCACCGACAAAGAATATCCTGTCAGACCAGCATACACACTAT
TAAACAAAATATTGGATGAATATTTAGTCGCACATCCTAAGGAAGAGTGGGCAGATGTGA
CTGAGACCAATGATGCATTGAAAATGAAGCAACTGGACACTTACATTAGCAAATATCAAG
ATCCTTCACAGGCTGACGCTATCATGAAAGTTCAACAAGAACTGGATGAGACGAAAATCG
TTTTGCACAAAACGATTGAGAATGTTTTACAAAGAGGTGAAAAGTTGGATAATTTGGTGG

ACAAATCGGAGTCATTAACGGCAAGTTCCAAAATGTTTTATAAGCAAGCTAAAAAATCCA
ATTCGTGTTGCATCATCATGTAG

>YKL196C, 200 aa (SEQ ID NO 254)
MRIYYIGVFRSGGEKALELSEVKDLSQFGFFERSSVGQFMTFFAETVASRTGAGQRQSIE
EGNYIGHVYARSEGICGVLITDKEYPVRPAYTLLNKILDEYLVAHPKEEWADVTETNDAL
KMKQLDTYISKYQDPSQADAIMKVQQELDETKIVLHKTIENVLQRGEKLDNLVDKSESLT
ASSKMFYKQAKKSNSCCIIM

>YKR076W, 1613 bp, CDS: 501-1613 (SEQ ID NO 259)
TAAATAGTTGAGGCTTTTCCTGCATTCTGTCAAGAAGGGTATGTGTATGAACATGCAAAT
GACACTGTAAAATGATTCATTACCCTGATTATGGAGTGATTTTCTTTCCTTTTTTTTTTT
ACATTTAGTTTCATTATTATGCAAATTAGAGGGTATACAGTTGAGATTTTAACACTTTGA
ATTAAAAAGTGTTACAGAGGAAACCGACGCAAAAGGCTTGGTGACGCAAACTTTTCCATC
TTTATTTCACCTCTTCAGACGGTCCTAAGACCTTTTGAACGTATCAATATAGTTTTATCA
TCTGTTCTCTGTTGTTCTCCGTTACTAAGATATTAGTCAGCTCTTGAAATTTCACACCCC
TATTTATTTGTCTTAGCGTCCAACCCCTCTCAACCCTTTTCCATTTCTTGTATAAAGGTA
GTTAATTAGGTAACGCTGCTCTTACCATCACTACAGTGCTTACGAGAATTTACCCAAACC
CTGCGCAAGATAAATAAGAAATGTCGAAACAGTGGGCGAGTGGTACAAACGGAGCTTTCA
AAAGACAGGTTTCGTCCTTCAGAGAAACAATCTCTAAGCAACACCCAATTTATAAGCCAG
CAAAGGGAAGATATTGGTTGTATGTTTCACTTGCATGCCCATGGGCCCATAGAACACTAA
TTACGAGGGCTTTGAAGGGATTAACCTCTGTTATAGGATGTAGCGTAGTCCATTGGCACC
TTGACGAGAAAGGATGGAGATTTTTGGACATGGAAAAGCAATTGGAGGACAGTGAAGATT
TTTTGGAACATTGGCACGATGTTGCAGGTGGTATTAGAACTGCTAAAGAGGATTCCAGCA
AGAGCTTCGCCGAGATCAAGAATGACAGTCAAAGATTCATGGTTGATGCTACCAATGAGC
CTCACTATGGATACAAGAGAATCAGTGACTTATATTACAAGAGCGATCCTCAATACTCGG
CAAGGTTCACCGTCCCAGTCCTGTGGGACTTAGAAACCCAAACAATTGTTAACAACGAAA
GTAGCGAAATTATAAGGATTTTGAACTCTAGTGCGTTCGATGAATTTGTCGACGACGATC
ACAAGAAACGGACCTTGTTCCTGCTCAGTTGAAAACACAGATCGATGACTTCAATTCTT
GGGTTTACGACAGCATCAACAATGGTGTATACAAGACCGGATTCGCAGAGAAAGCAGAAG
TTTACGAAAGTGAAGTCAACAACGTATTTGAACATTTGGAGCAAAGTGGAGAAAATCCTGA
GTGACAAATATTCCAAATTGAAGGCCAAATACGGTGAAGAAGATAGACAAAAAATCTTGG
GTGAGTTCTTCACTGTGGGTGATCAATTAACAGAAGCTGACATTAGATTGTATACTACCG
TCATAAGATTCGATCCTGTGTACGTCCAACATTTCAAATGCAATTTTACCTCTATTAGAG
CCGGATATCCATTTATTCATTTGTGGGTAAGAAATTTATACTGGAATTATGATGCCTTCA
GGTACACAACAGATTTTGACCATATCAAGTTACACTACACGCGTTCCCACACAAGGATCA
ACCCCTTGGGAATTACGCCCCTGGGACCCAAGCCAGATATTCGTCCTTTATAA

>YKR076W, 370 aa (SEQ ID NO 260)
MSKQWASGTNGAFKRQVSSFRETISKQHPIYKPAKGRYWLYVSLACPWAHRTLITRALKG
LTSVIGCSVVHWHLDEKGWRFLDMEKQLEDSEDFLEHWHDVAGGIRTAKEDSSKSFAEIK
NDSQRFMVDATNEPHYGYKRISDLYYKSDPQYSARFTVPVLWDLETQTIVNNESSEIIRI
LNSSAFDEFVDDDHKKTDLVPAQLKTQIDDFNSWVYDSINNGVYKTGFAEKAEVYESEVN
NVFEHLDKVEKILSDKYSKLKAKYGEEDRQKILGEFFTVGDQLTEADIRLYTTVIRFDPV
YVQHFKCNFTSIRAGYPFIHLWVRNLYWNYDAFRYTTDFDHIKLHYTRSHTRINPLGITP
LGPKPDIRPL

>YKR092C, 1721 bp, CDS: 501-1721 (SEQ ID NO 261)
TCAAGGATACCTGGTTGATTCTACGTCGTCCTCTTCACTTTGGTTAATTCACCTTTGCCC
TTCACCTTGTGGTGTGCGGGTGTTGCAGTCATTAATGTTCTTTATCGCGAGAGGGGGTCT
ACATAATCTTTGTTTTTTCACTCCAATAAGGCAGTTATAGTGAATTTGTTTTATTACAGAA
GGTGTACCCTTCGTTCGAGTTATTTACTCTTGTTTTGTAGTTTGTACATCTCTTTATGT
CTGGATCAAAACGATAATTCGAAGCTTATTGCAATTTAGTTCTCTTACCCATTTCTTTAC
AACGGGCCGAGAAAAAGTGGAGTTGGTCCGAGGAAGCTTTGAACGGGAAGAGGAAAAAAC
CTTCCCATCGCTCGAGCATACAATTTTTTTTTTTTCAATGCAGGCTGAAAAAAAAAAATT
CACTTGATGATTGAACTCATCGCACTTTTATACAAAGCAAGAAAGAAACCCAAGTCGCAG

TACACTAAGAATACATAGCAATGGCTTCCAAGAAAATTAAAGTTGACGAAGTGCCAAAAT
TAAGTGTTAAGGAGAAGGAGATTGAAGAGAAATCTTCTTCTTCTTCTTCCTCCTCCTCCT
CCTCCTCCTCCTCCTCTTCTTCTTCATCTTCCTCGTCCAGTTCTAGCGGCGAATCTTTCAA
GCAGCAGCAGCAGCAGCAGCAGCAGCAGTGACAGCAGTGACAGCAGTGACTCTG
AATCTAGCTCATCATCATCTTCTTCTTCTAGCTCAAGCTCAAGTTCCAGTGACTCTGAAT
CTTCTAGTGAATCCGACTCTAGCTCCAGTGGATCTTCTTCTTCCTCTAGCTCTAGTTCTG
ACGAATCTTCTTCGGAATCCGAATCAGAAGATGAAACCAAGAAAAGAGCAAGAGAATCAG
ACAACGAAGATGCTAAGGAGACTAAAAAGGCTAAAACTGAACCAGAAAGCTCTTCCTCAT
CGGAGTCAAGCTCTAGCGGGTCATCGTCATCTTCAGAATCAGAATCAGGTTCGGAATCTG
ATTCTGACTCAAGTTCTAGCTCAAGTAGTTCTTCTGATTCCGAATCAGATTCTGAATCAG
ATTCTCAATCAAGTTCTAGCTCCAGCTCTAGCGACTCTTCGTCTGACTCCGACTCCAGCT
CCAGCGACTCTTCATCTGACTCCGACTCTAGCTCCAGCTCTAGCAGCTCTTCCTCGGATT
CAGATTCCGGATTCCGACTCAAGCTCGGACTCAGACTCTTCAGGCTCGTCCGATTCTTCAA
GCTCGTCTGATTCAAGTTCCGACGAATCTACATCTTCTGATTCCTCCGATTCGGATTCCG
ACTCAGACTCTGGTTCTAGCTCTGAATTGGAAACAAAAGAAGCAACTGCAGACGAATCCA
AGGCCGAAGAAACGCCTGCCTCATCTAACGAATCAACTCCATCTGCTTCCAGTTCATCAA
GCGCCAATAAATTGAACATTCCTGCTGGAACCGACGAGATCAAAGAGGGCCAAAGAAAGC
ATTTTTCCAGAGTAGATAGATCGAAGATTAATTTCGAAGCTTTGGGAGTTGACAGACAACA
CCTACAAAGGCGCGGCTGGAACATGGGGTGAAAAGGCAAATGAAAAATTAGGTAGAGTAA
GAGGTAAAGATTTCACGAAGAACAAAAATAAAATGAAGAGAGGTTCTTACAGAGGTGGAT
CCATTACATTAGAAAGTGGTTCATACAAATTCCAAGATTAA

>YKR092C, 406 aa (SEQ ID NO 262)
MASKKIKVDEVPKLSVKEKEIEEKSSSSSSSSSSSSSSSSSSSSSSSSGESSSSSSSSS
SSSSSDSSDSSDSESSSSSSSSSSSSSSSSSDSESSSESDSSSSSGSSSSSSSSSSDSESSES
ESEDETKKRARESDNEDAKETKKAKTEPESSSSSESSSSGSSSSSESESGSESDSDSSSS
SSSSSDSESDSESDSQSSSSSSSDSSSDSDSSSSDSSDSDSSSSSSSSSSDSDSDSDS
SSDSDSSGSSDSSSSSDSSSDESTSSDSSDSDSDSDSGSSSELETKEATADESKAEETPA
SSNESTPSASSSSSANKLNIPAGTDEIKEGQRKHFSRVDRSKINFEAWELTDNTYKGAAG
TWGEKANEKLGRVRGKDFTKNKNKMKRGSYRGGSITLESGSYKFQD

>YLR043C, 812 bp, CDS: 501-812 (SEQ ID NO 269)
AGACAAGTCTTTCAACGACAACTCTAAGATCAGAATGATTGAAATCATGTTGCCAGTCTT
CGATGCTCCACAAAACTTGGTTGAACAAGCTAAGTTGACTGCTGCTACCAACGCTAAGCA
ATAAGCGATTTAATCTCTAATTATTAGTTAAAGTTTTATAAGCATTTTTATGTAACGAAA
AATAAATTGGTTCATATTATTACTGCACTGTCACTTACCATGGAAAGACCAGACAAGAAG
TTGCCGACAGTCTGTTGAATTGGCCTGGTTAGGCTTAAGTCTGGGTCCGCTTCTTTACAA
ATTTGGAGAATTTCTCTTTAAACGATATGTATATTCTTTTCGTTGGAAAAGATGTCTTCCA
AAAAAAAAACCGATGAATTAGTGGAACCAAGGAAAAAAAAAGAGGTATCCTTGATTAAGG
AACACTGTTTAAACAGTGTGGTTTCCAAAACCCTGAAACTGCATTAGTGTAATAGAAGAC
TAGACACCTCGATACAAATAATGGTTACTCAATTCAAAACTGCCAGCGAATTCGACTCTG
CAATTGCTCAAGACAAGCTAGTTGTCGTAGATTTCTACGCCACTTGGTGCGGTCCATGTA
AAATGATTGCTCCAATGATTGAAAAATTCTCTGAACAATACCCACAAGCTGATTTCTATA
AATTGGATGTCGATGAATTGGGTGATGTTGCACAAAAGAATGAAGTTTCCGCTATGCCAA
CTTTGCTTCTATTCAAGAACGGTAAGGAAGTTGCAAAGGTTGTTGGTGCCAACCCAGCGG
CTATTAAGCAAGCCATTGCTGCTAATGCTTAA

>YLR043C, 103 aa (SEQ ID NO 270)
MVTQFKTASEFDSAIAQDKLVVVDFYATWCGPCKMIAPMIEKFSEQYPQADFYKLDVDEL
GDVAQKNEVSAMPTLLLFKNGKEVAKVVGANPAAIKQAIAANA

>YLR053C, 827 bp, CDS: 501-827 (SEQ ID NO 271)
AACACTGGGGATATTTTGAGATTTACCACTAGTAGATACGGTGGTGTAGATACGTATGAT
TCCATCTTGAGGGACCAATCCACGATCATGGAACTTTTAGATAAACGGTGTGCCTATTCA
CCTCCAGTACTGTTCGATAATGAGGCTAAAGAACGTGATCATGATCGCGATTGTTATCAA
GATTACAATCACGACCACCGGAGTCATTAATATTAAAAAAAAAAAATGTGATTGTTAATA

AGGGGTGGGATGCGCGAAATTCTATGCCTACAGTAGAAAGCGGTTGTTGCACAAATGATT
AAATCTTTATCTCCAACTCACAATACTATCGCGATAGATGCATAAATATGTGCAGCTTCTA
AACAGCACGGAGTGATGATAAATACGCATATATGTATATATATATGTATGTGCATATGCA
CGTCCTTTTAAAACTCAAAATACAACATTCTTAGTAAATCCTTTTGTTGACACACGTCGG
AACAACTCAGGACGGAGTTAATGGATATGCTTCATAATAAATGTAGTGATGCTATCAAAA
GCACCTCCAATAGCAATTTGAGTAATGAGGTAGACAAACAAAAATTGCAATACGATGACC
TCGGGAACACCGGATTTTCTGAACTATTTGAGATGGAATCTCAAGATAATAATGATAGCA
TAGAGGATTTCTTGTTCTTTAATATAAATTTAACCCAGGAGGTTGAGTTCGAGAACCAAA
GACAATATGAGCACACGAAAAAGACAAAGAAGCATAACCCATTCTATGTACCGTCAGAGG
TAGTGCGAGAGATGGTCAAGAAACACGCATTGAATGGCAGAATATAG

>YLR053C, 108 aa (SEQ ID NO 272)
MDMLHNKCSDAIKSTSNSNLSNEVDKQKLQYDDLGNTGFSELFEMESQDNNDSIEDFLFF
NINLTQEVEFENQRQYEHTKKTKKHNPFYVPSEVVREMVKKHALNGRI

>YLR390W, 839 bp, CDS: 501-839 (SEQ ID NO 291)
GTGAAATTGAGACTGATAGGTGAGAGGTGAACCAATTGAGTGAGGAGTGGTTTAGTTACA
AATGCAGAAGAAGAAGCTAAAAGAGATACGCCCATACAGAGCAATATCAAAATGAGCAAG
AATGAGGTCTTCCGAATGGTTGGTTCTGACTTACTATTTGATTTCACTTTCTCTGATTCA
TTCAGGAAGAAAAGGGCGAAGTCCTCGAAATGAAAATTTCAACATCATTAACAGACCGGC
GCGCGCCTTTACAATTTAGTATGTACGCCACCAATAAAAGCTGCTTAAACAATAAGCTAG
AAAGCCCAAAGGGTCTTAAATAGTACAGCGAACCCTTCAGCAACGGTACATCAACAACCC
CTTGAAAAGAATAGAGACAATACAGCTACAGTCATCCCCTTCTCTTGTATTTTTGGCCAC
AATTGATTGTATTACATCATATTTTGCCTGTGCGCTTCTTCTATCTTTTCCGCATAAACT
AGGGGAAACGCGATGAAGAAATGGATTGGCTGAAAAATACAACAATTGTAGTGTTATTCA
GTCATTCAACTGACAAAAGTAACAAACACAAGAAACGTCAAGTCCAGTGCAATATGCGAA
AGAACACTTTAGATATGGTCACTATAGGTATCGCATGCCTTGTGGGAGTCTACACGGGCA
CGAGATTTTTCGAGCCCATTGTTATCGATAGATTGCGTAAGGATGGAAACTTGAGAACGG
ACATTCCCATCCCAGAATACGACGAGGACGGAAATCTGTTAAAGGTCACGCCGTCTTTAT
CATCCACACCAGCTGCACCACCTACACCACCTACACCTCCTACTCCACCACAACAGTAA

>YLR390W, 112 aa (SEQ ID NO 292)
MDWLKNTTIVVLFSHSTDKSNKHKKRQVQCNMRKNTLDMVTIGIACLVGVYTGTRFFEPI
VIDRLRKDGNLRTDIPIPEYDEDGNLLKVTPSLSSTPAAPPTPPTPPTPPQQ

>YMR251W, 1601 bp, CDS: 501-1601 (SEQ ID NO 315)
ACTCCAGAGCGCAAGAGTTCGTTCATCTACGAAATGTTGCTGGCATTGGCATCTCCACAA
GATGACATCCCAACGCCGGATGAAATCGAAAAGAAAAATAAGCTAAAGGAAACAACAACG
AGAAACTATAGAGGAACATGTTGAGTTGAAAAGGTCATCCAATATACCGCCCCCTATATG
TATGTACCTTTACCTTTATTTAAGTACTAGTGCTGTTTAGTTAGGTTATGTGAAGGCAC
GGGTTTTGTCTTTTTTTTTTTTTTTTTTTACTATTACTTTCTTTTCAAGCTTTTAAGCG
CCGAAATGATATTTAAGGGAAGATGACTAAAGGGACAGCGACGAGGATTCAGCCTGGACA
GTGATAGAAAAGTTATGCGGGAATACGTATATATAGTTGTATAAATTGTGGTTATAGAAC
ATCGCAGCGCCTTTAAATATATTGTCTTTTATTTCAATCTTATTCCATCTCTCTCTTGCA
ACCACGGCAAAGCTGGAGCTATGTCTGAAAAATCAGCTAGCAATAACAAAGCTGAATTCA
AAAGGCAGTCATCGCCATTCAGAGAAATCATCTCTGCGGATCACCCAATTTATAAACCTG
CTAAGGGAAGGTACTGGCTGTATGTGGCGCTACCATGCCCATGGGCACAAAGAACCTTGA
TCACCAGGGCCCTGAAAGGGCTAGCGCCTATAATCGGGTGCAGTGTAGCGCATTGGCACC
TGGATGACAAAGGCTGGCGATTCCTTGAAGAAGGAGATGGGAAAACCAATGAAAGGCACT
GGTTTGACATTGCAGGCGGAATTAGCTCAGTAAATTTAAATACCAGTACTCCTGTGGCTA
ACATACCCAATAACGCGCATCGGTTGTTGGTCGACGGAACAGATGAACCGCATTACGGGT
ACAAGAGACTAAGCGACTTCTATTTCAAAACAAAGCCAGACTATAAGGGAAGATTCACCG
TACCTGTTCTTTGGGACTTGGAAACATGCACTATAGTAAACAATGAAAGCAGTGATATCA
TCGGAATTATGAATTCCGCTGCGTTTGATGAGTTTGTCGGCGAAGAATACCGTCAAGTCC
GTCTGGTACCTCGGTCTCTAGAGGCACAGATTACAGAGTTCCAACTCTTGGGTGTACGATA
AAATCAACAACGGTGTATACAAGGCCGGTTTTGCAGAATGTGCAGAGGTATACGAGAGGG

AGGTAACAAGCCTTTTTCAATATCTTGACAAATTGGAAAATCTTCTGGACAAGAAGTACA
CAGATTTGGAGGCGGAGTATGGTAAGAACAACAAGGACAAGATACTAGATCGCTACTTTG
CCATCGGAGACACTCTGACCGAGGCGGACGTGAGACTCTACCCAACGATAGTAAGGTTCG
ACGTGGTATACCATCAACACTTCAAATGCAATCTGGCCACCATCAGAGATGATTATTCCC
GTATACACACGTGGCTCAAGAATATATACTGGCGCCACGAAGCCTTCCAGCGCACAACGG
ACTTTACCCACATAAAACTCGGATATACTCGCTCGCAGCCACGGGTCAACCCGATTGGGA
TCACCCCACTGGGGCCCAAGCCTGATATCCGACCTCCATGA

>YMR251W, 366 aa (SEQ ID NO 316)
MSEKSASNNKAEFKRQSSPFREIISADHPIYKPAKGRYWLYVALPCPWAQRTLITRALKG
LAPIIGCSVAHWHLDDKGWRFLEEGDGKTNERHWFDIAGGISSVNLNTSPVANIPNNAH
RLLVDGTDEPHYGYKRLSDFYFKTKPDYKGRFTVPVLWDLETCTIVNNESSDIIGIMNSA
AFDEFVGEEYRQVRLVPRSLEAQITEFNSWVYDKINNGVYKAGFAECAEVYEREVTSLFQ
YLDKLENLLDKKYTDLEAEYGKNNKDKILDRYFAIGDTLTEADVRLYPTIVRFDVVYHQH
FKCNLATIRDDYSRIHTWLKNIYWRHEAFQRTTDFTHIKLGYTRSQPRVNPIGITPLGPK
PDIRPP

>YMR273C, 3248 bp, CDS: 501-3248 (SEQ ID NO 321)
AAATTGGTCTCAATCTGGAATAAGTGCTACTTCGCACTGCTGGTCCTTGGATTAATATCC
CTGAAGGATACCTTACAAACTCTGGTAGGAACTCCTGGTTATAGAATAACCCTTTAGCCT
TTTTTACGTACTTGTATACCGTTTAAAATTTCCTATGTACTATAACCTTTTTTCACTACT
ATTATGGAATTCTATCGAGCGACCGGGCTTTTGTTACGGAAGAGTGAAAAAATCGAGTTT
TGGTGTTTTGGTGAAAGAATTTGGAGGACTATAAAGTACCTATACTTTGTATTACGGACT
CAATAACAAGTCGTTCGTGTCAGTGGTATTGAAGTTGTCAGATCTAAGAGTAGAGAGAAG
GTGGCATCTAATAGGTTTCGACGTTTTTCTTTTTTTAAGGTTTTATTTGGTCCTCCTAGA
ATTTAAGGTCTTAGTTAGTTTTGGTTTGTTTTGTGGGTTACATATTTTCAATTCAAAGGA
GAATTTAGCTGTCTTTTATAATGTCCAATAGAGATAACGAGAGCATGCTGCGTACTACAT
CAAGCGATAAGGCGATCGCTAGTCAAAGGGATAAACGGAAGTCTGAAGTTTTGATTGCTG
CACAGTCCCTTGACAATGAAATCCGCAGCGTAAAAAACCTAAAAAGATTGTCGATTGGGT
CAATGGATTTACTTATTGATCCAGAATTAGATATAAAATTCGGTGGGGAATCTAGTGGGA
GACGATCATGGTCTGGCACGACATCCAGTTCTGCGTCAATGCCAAGTGACACAACCACCG
TTAATAACACACGATATAGCGATCCAACTCCGCTAGAGAACTTGCATGGGAGGGGTAACT
CAGGGATAGAATCCTCCAATAAGACTAAACAAGGTAACTACTTAGGTATAAAAAAAGGTG
TTCACTCTCCATCCAGGAAATTAAATGCTAACGTATTAAAGAAAACTTATTATGGGTTC
CCGCCAATCAACACCCTAACGTTAAGCCTGATAATTTCCTAGAGCTTGTACAAGATACTT
TACAAAATATACAACTAAGCGACAATGGTGAAGATAATGATGGGAATAGCAATGAAAATA
ACGATATTGAGGATAATGGGGAGGATAAAGAATCACAATCATATGAAAATAAGGAGAACA
ACACTATCAACTTGAACAGGGGGCTGTCAAGGCATGGAAACGCGTCACTAATACGAAGGC
CTTCAACATTGCGGAGGTCATATACAGAGTTTGATGATAACGAAGATGACGATAATAAGG
GAGACAGTGCCTCTGAAACAGTAAATAAAGTCGAAGAAAGAATCTCCAAAATAAAAGAGA
GACCAGTGTCGTTAAGAGATATAACTGAAGAACTGACAAAGATCTCAAATAGTGCAGGAC
TAACCGACAATGATGCCATTACATTAGCCAGAACTCTTAGTATGGCTGGTTCATATTCAG
ATAAAAAAGATCAACCACAACCGGAAGGGCATTATGATGAAGGAGATATTGGTTTTTCAA
CTTCACAAGCGAATACTTTGGATGATGGTGAATTTGCCTCCAATATGCCCATCAATAATA
CCATGACATGGCCTGAACGATCGTCACTGAGAAGGAGTAGATTCAACACTTATCGAATCA
GGTCACAAGAGCAAGAAAAAGAAGTAGAACAAAGTGTGGATGAAATGAAAAACGACGACG
AAGAACGTCTAAAATTGACCAAGAATACAATAAAGGTCGAAATAGATCCGCACAAATCCC
CTTTTAGACAGCAAGATGAGGATTCTGAGAATATGAGTTCGCCTGGGTCAATTGGTGATT
TTCAAGACATTTATAATCATTACAGACAGTCTAGTGGCGAGTGGGAACAAGAAATGGGAA
TAGAGAAAGAAGCCGAAGAGGTACCCGTCAAGGTTCGAAATGACACAGTAGAACAAGACT
TAGAGTTAAGAGAGGGAACAACAGACATGGTAAAGCCAAGCGCAACGGATGACAACAAAG
AAACGAAGCGACATCGTCGAAGAAACGGATGGACATGGTTGAACAATAAAATGAGCAGAG
AAGACGATAACGAAGAAAACCAAGGGGACGATGAAAATGAAGAAAACGTGGATTCACAAA
GAATGGAGCTCGACAATTCCAAAAAACATTATATTTCTCTATTTAATGGCGGTGAGAAGA
CGGAGGTGTCAAATAAAGAAGAAATGAACAATTCAAGTACTTCCACCGCCACATCACAGA
CAAGACAGAAAATCGAGAAAACTTTTGCGAACCTATTCAGAAGAAAGCCACACCACAAGC

ATGATGCATCATCATCACCCTCGTCGTCACCATCATCGTCACCATCAATACCAAATAACG
ATGCCGTGCACGTTCGCGTGAGGAAAAGCAAAAAGCTTGGTAACAAAAGTGGAAGGGAGC
CGGTTGAACCCATTGTGTTGCGCAATCGCCCTCGTCCTCACCGTCACCATCACAGCCGTC
ATGGTTCCCAAAAAATAAGCGTAAAAACCCTTAAAGATTCTCAGCCGCGACAGCAGCAGATAC
CATTACAACCACAATTGGAAGGCGCAATAGAGATAGAAAAGAAAGAGGAAAGCGATTCCG
AGAGCTTGCCCCAACTACAGCCGGCCGTTAGTGTAAGTAGTACCAAAAGTAACTCTAGAG
ACAGAGAAGAAGAGGAGGCAAAGAAAAAGAACAAGAAGAGGAGCAATACGACAGAAATTT
CCAACCAACAACACTCCAAACACGTCCAAAAGGAGAATACCGATGAGCAAAAAGCTCAAC
TACAAGCTCCAGCTCAAGAACAAGTCCAAACTTCAGTCCCAGTTCAAGCTTCAGCCCCAG
TCCAAAATTCAGCCCCAGTCCAAACTTCAGCCCCAGTTGAAGCTTCAGCTCAAACTCAGG
CTCCAGCGGCACCACCATTGAAACATACCTCCATATTGCCCCCAAGAAAGCTTACATTTG
CAGACGTCAAAAAACCTGACAAACCAAACTCCCCGGTTCAATTCACAGACAGTGCCTTTG
GGTTCCCACTGCCTTTGCTGACAGTGTCTACGGTTATTCATCGTTCGACCACCGTCTACCAA
TTAACGTCGAAAGGCCCATATACCGGCTGAGTCACTTGAAATTGAGCAATTCGAAGAGGG
GACTGCGCGAGCAGGTATTACTAAGTAACTTCATGTATGCTTATCTGAACTTGGTTAATC
ACACTCTGTACATGGAGCAGGTAGCCCACGACAAAGAACAACAACAACAACAACAACAAC
AACCCTGA

>YMR273C, 915 aa (SEQ ID NO 322)
MSNRDNESMLRTTSSDKAIASQRDKRKSEVLIAAQSLDNEIRSVKNLKRLSIGSMDLLID
PELDIKFGGESSGRRSWSGTTSSSASMPSDTTTVNNTRYSDPTPLENLHGRGNSGIESSN
KTKQGNYLGIKKGVHSPSRKLNANVLKKNLLWVPANQHPNVKPDNPLELVQDTLQNIQLS
DNGEDNDGNSNENNDIEDNGEDKESQSYENKENNTINLNRGLSRHGNASLIRRPSTLRRS
YTEFDDNEDDDNKGDSASETVNKVEERISKIKERPVSLRDITEELTKISNSAGLTDNDAI
TLARTLSMAGSYSDKKDQPQPEGHYDEGDIGFSTSQANTLDDGEFASNMPINNTMTWPER
SSLRRSRFNTYRIRSQEQEKEVEQSVDEMKNDDEERLKLTKNTIKVEIDPHKSPFRQQDE
DSENMSSPGSIGDFQDIYNHYRQSSGEWEQEMGIEKEAEEVPVKVRNDTVEQDLELREGT
TDMVKPSATDDNKETKRHRRRRNGWTWLNNKMSREDDNEENQGDDENEENVDSQRMELDNS
KKHYISLFNGGEKTEVSNKEEMNNSSTSTATSQTRQKIEKTFANLFRRKPHHKHDASSSP
SSSPSSSPSIPNNDAVHVRVRKSKKLGNKSGREPVEPIVLRNRPRPHRHHHSRHGSQKIS
VKTLKDSQPQQQIPLQPQLEGAIEIEKKEESDSESLPQLQPAVSVSSTKSNSRDREEEEA
KKKNKKRSNTTEISNQQHSKHVQKENTDEQKAQLQAPAQEQVQTSVPVQASAPVQNSAPV
QTSAPVEASAQTQAPAAPPLKHTSILPPRKLTFADVKKPDKPNSPVQFTDSAFGFPLPLL
TVSTVIMFDHRLPINVERAIYRLSHLKLSNSKRGLREQVLLSNFMYAYLNLVNHTLYMEQ
VAHDKEQQQQQQQP

>YNL112W, 3143 bp, exon1: 501-1773, intron1: 1774-2775, exon2: 2776-3143 (SEQ ID NO 327)
CTTGATGGATTTATGTGACGTTGTAGAATCTAAGTTTACTGAAAAAATCAAGAGCATGTA
GATGTTACGGATCGACTCAAAGACCCTCTGTCACTCTGAAATTTCTAATAATTATGCACA
CCACGCTAGTATAGATACAGCTTGATTTGTGTATCCCGTTTATAGTCGTGCTATTTAAAA
TCTATGTATAATATAACCAGATAAAAATACACCTTCGTACAAGGTGCTAATAATGTTGAG
AATTCGAAATTCCTTTTTAAAGGCGTATTCCGTATTGAATGATTGAAAAATTTATTTCTT
TTTTTATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTACGCCGATGCTCATCGCAGAAAAT
TTTTCCTTCAGTTTATTTGTCTTATAAAAAGACTGTCCTACGCTCAAATAACTTATACTT
TTCTGTATCTCATTCAAATTATTTTCTTGTCAACAACCTGTAACAGAATTAAGCACTATT
AAGGCAAATTTAGAGCAAATATGACTTACGGTGGTAGAGATCAGCAATATAACAAGACTA
ACTACAAGTCTAGAGGTGGCGACTTCCGCGGTGGAAGAAACTCTGATAGAAACTCTTACA
ATGACAGACCACAAGGCGGTAACTACCGTGGTGGTTTCGGTGGTCGTTCCAATTACAACC
AACCCCAGGAATTGATCAAACCAAACTGGGATGAAGAATTACCCAAATTGCCAACTTTCG
AAAAGAATTTCTATGTTGAACACGAAAGTGTTCGCGACAGATCGGACAGTGAGATTGCTC
AGTTCAGAAAGGAAAATGAAATGACTATTTCCGGACACGATATTCCAAAGCCAATCACCA
CTTTCGATGAAGCTGGTTTCCCAGACTACGTTTGAATGAAGTGAAGGCTGAAGGATTTG
ACAAACCAACTGGCATTCAATGTCAGGGTTGGCCAATGGCTTTATCTGGTAGGGACATGG
TTGGTATTGCTGCCACTGGTTCCGGTAAGACTTTGTCTTATTGTTTACCAGGTATTGTTC
ATATCAACGCTCAACCATTATTGGCTCCAGGCGATGGACCAATTGTTTTGGTTTTGGCTC

CAACTAGAGAATTGGCTGTTCAAATTCAAACAGAATGTTCCAAGTTTGGTCATAGTTCCA
GAATCAGAAATACCTGTGTCTACGGTGGTGTTCCAAAAAGTCAACAAATCAGAGATTTAT
CTCGTGGCTCTGAAATTGTTATTGCTACTCCAGGTCGACTAATTGATATGCTAGAGATTG
GTAAGACTAATTTGAAGAGAGTCACTTACCTGGTTCTTGATGAAGCTGATAGAATGTTAG
ATATGGGTTTTGAACCTCAAATCAGAAAGATTGTTGATCAAATCAGACCTGATAGACAAA
CCTTGATGTGGTCTGCCACTTGGCCAAAGGAGGTGAAGCAACTAGCCGCTGATTACTTGA
ATGATCCAATTCAAGTTCAAGTTGGTTCTCTAGAACTATCTGCCTCCCATAATATTACTC
AGATCGTCGAAGTTGTTTCTGATTTCGAAAAGAGAGATCGTTTGAACAAGTACTTAGAAA
CAGCCTCTCAAGACAACGAATACAAGACATTAATCTTTGCTTCTACGAAAAGAATGTGCG
ATGATATCACCAAGTATCTAAGAGAAGATGGATGGCCCGCCTTGGCTATTCATGGTGACA
AAGACCAAAGAGAACGTGACTGGGTTCTACAAGAGTTTAGAAACGGTAGATCCCCAATTA
TGGTTGCTACTGATGTGGCCGCCAGAGGTATCGGTATGTTAAAATTTTCTCCATTTTTTT
ATTGATTTTATTTTTTTTTGTTACCCCTAACGATATTACAGCTATTTCCCTAATGGCTTTT
AATGACATTAATGACTTTATGACAACCATGATAGTACAGAAGAAGAGACCTTTTTCTTTT
TTTTTTTTTTTTCTTTTTTTTTTTTTTTTCTTTTTTTCTTTTTTTTTTTTTTGAGCCTTT
TCGAATCTAGACTCTATGTGAGTCTATTCTCGATGGGAGTATCGGAAATTGAATTTTAA
TTCGAATGACTTCTAATGCATCACTACAGAAAACTAATATTGGGAGGATGAGAAAAATTG
ACTTTAATTAGTCGTTTTGAGAGACGGGAAATTATAAACTCGGAGAAGTGTATTTGTGTT
CATGATTTGCACTTCATGTCAAAAGAAATTTCGCTTTTTGACATCGGCGCAAATAAACAA
GGAATTGGCTTTTCAGCTTATTTCTAGAACGCATACATCAGCTTCGTTGATCGTTGTTTT
TTTCAATGCTTGGCATTTGTACAAGGGTAGATTGTTTTATTGGAAAAATAATAGTATATT
CTACTTTGAAATGCCGTCATCCTTCTTGACTATTGTTATTCTCATTTTGTGTAGTTTATG
CATTTTGTAGTTATATTGAGATACTGTTGCATCCCAAGTTCGAATTATTAAGAAGTGCTG
ATAAAAATGGAAAATAACAAAATAAAAGGATTTCAACCATATTCAGAAATCATTTACTTT
GTTTTCCTTTTTTTAAGTGCTAGCTTTCATTCAGTTTGAATAAGGATTCTGGAGTATTGA
TGATTAAATATTTCGAATTCTTTAATAAAAATATAATTTCTGATAATCTTCAAGCCAGGG
GGAAATTTGAGACAATGTTGGGAGTCCAAACATGAATTTGTGGGGGGCATGAAAATAAAG
TTCATATACAGAATAACGAACCAAATTACTAACAGTATGCTTTGTAAACGTTTGTTTACT
TCTTTATTTTTTCAGATGTCAAAGGTATCAATTACGTTATCAACTACGATATGCCAGGTA
ACATTGAAGATTATGTTCACAGAATCGGTAGAACTGGTAGAGCAGGTGCTACTGGTACTG
CTATATCTTTCTTCACCGAACAAAACAAAGGTTTAGGTGCTAAATTAATCTCTATCATGA
GAGAAGCTAATCAAAATATTCCTCCCGAATTATTGAAATACGACAGGAGATCTTATGGTG
GCGGTCACCCAAGATACGGTGGTGGTCGTGGTGGTCGTGGTGGCTATGGCCGTAGAGGTG
GTTACGGTGGTGGCCGTGGTGGTTACGGCGGTAACAGGCAGAGAGATGGTGGCTGGGGTA
ACAGAGGTCGTTCAAACTATTGA

>YNL112W, 546 aa (SEQ ID NO 328)
MTYGGRDQQYNKTNYKSRGGDFRGGRNSDRNSYNDRPQGGNYRGGFGGRSNYNQPQELIK
PNWDEELPKLPTFEKNPYVEHESVRDRSDSEIAQFRKENEMTISGHDIPKPITTFDEAGF
PDYVLNEVKAEGFDKPTGIQCQGWPMALSGRDMVGIAATGSGKTLSYCLPGIVHINAQPL
LAPGDGPIVLVLAPTRELAVQIQTECSKFGHSSRIRNTCVYGGVPKSQQIRDLSRGSEIV
IATPGRLIDMLEIGKTNLKRVTYLVLDEADRMLDMGFEPQIRKIVDQIRPDRQTLMWSAT
WPKEVKQLAADYLNDPIQVQVGSLELSASHNITQIVEVVSDFEKRDRLNKYLETASQDNE
YKTLIFASTKRMCDDITKYLREDGWPALAIHGDKDQRERDWVLQEFRNGRSPIMVATDVA
ARGIDVKGINYVINYDMPGNIEDYVHRIGRTGRAGATGTAISFFTEQNKGLGAKLISIMR
EANQNIPPELLKYDRRSYGGGHPRYGGGRGRGGYGRRGGYGGGRGGYGGNRQRDGGWGN
RGRSNY

>YNL131W, 959 bp, CDS: 501-959 (SEQ ID NO 329)
CAAAAAGAGCTAATCAACTCCTTGAACTTAGATAAATACGCCATAAATGATAACAGTGAG
GAATGGGCTGAATCTCAAAAATCTTTAGAAATAGCTGCCAAGGCCAAAGGCGTCGTCAGT
TTAAAAACTGGTAAAAAGAGAACGACTGAAAAGGCTGAAGATATCTATAGACAAGAGATG
AAAGCTATGAAAAAACCAAGAAAGTCTAAAAAGGCTGCAAATTAAGCGTTCTACTCTTTG
TCAAACCCTTTTATAGCTAAACGTTTACTTAATTTGTACAATAATATAGAATAGAAACAT
AGTTGATGTTTGAACCTTTACATATTCCTTTCAATCGTGTCGAGCGATATAAGTATTACG
ATTATGCCGGCGAAAACTGAACCCGTTTTAGACAATTTCAATCAACATACTCCACTCCGT

AGTGAGTAACTTTTGGAGTAATACGAAGTAACCAAAGAGGTCAAAACGGAACTATATACC
CCAAAATAAGCATCATTCAAATGGTCGAATTAACTGAAATTAAAGACGATGTCGTTCAAT
TAGACGAACCACAATTTTCCAGAAATCAGGCCATCGTGGAAGAAAAGGCTTCTGCAACAA
ACAACGACGTTGTCGATGATGAAGATGACTCTGATAGTGATTTTGAAGATGAATTTGATG
AAAATGAAACATTGTTGGACAGAATCGTTGCTTTAAAAGACATTGTCCCCCCAGGTAAGA
GACAAACAATTTCTAATTTTTTTGGTTTTACTAGCTCTTTTGTGAGAAATGCTTTCACAA
AATCCGGAAACCTTGCTTGGACTTTGACCACCACTGCTTTGTTACTCGGTGTGCCACTAT
CCTTATCTATACTTGCCGAACAACAGCTAATCGAAATGGAAAAGACATTTGATTTACAAA
GTGATGCTAATAACATATTGGCCCAAGGTGAAAAAGATGCTGCAGCAACAGCCAATTAA

>YNL131W, 152 aa (SEQ ID NO 330)
MVELTEIKDDVVQLDEPQFSRNQAIVEEKASATNNDVVDDEDDSDSDFEDEFDENETLLD
RIVALKDIVPPGKRQTISNFFGFTSSFVRNAFTKSGNLAWTLTTTALLLGVPLSLSILAE
QQLIEMEKTFDLQSDANNILAQGEKDAAATAN

>YNL143C, 893 bp, CDS: 501-893 (SEQ ID NO 333)
GAAAATACACACGGCGGAAGCCATCATCGAGGCCCAAAGCAAGGATAAAGCATGCTTTTT
CCTGGATAAACCAGAATATAATAAACCGATACCTGGGACCATAATCCACACACCTGCTGA
AGCCACACCGATCCATCCCATGTTGGCCAAGTCAAATTGTGTATTCAAATCTGTTGTCAA
CGAGTTACCACCCGTTCCTTCGCCTGTAGGCGTACCTGTAAAATTGTAAGACATTGTTGA
TATTGTATTGTAATATATTAAGTATGATATATTACAAAACTAAACTTCTTTCAAAGCTCT
GTGCAGACTTATTATTTTAAGAAGGATATTTAATTTGAAAGGACGTGAAAGCACGAATGAT
TACTACCCACTGATGTTTGGTTAGCACATGTGTAACTACTGCTTATATATGGTGCAGAAA
AGTGGCTCGGAATGAACACCTCTTGTACTGAATACTTCATTGATAAGGCACAGGGTCTTC
ACGCCGCTTAGTATTCGTCGATGCGTGAGCAATTGAAGCTTTTTACGAGGGAAATAGTCG
ATTTTACATTTCTTATCTTATCTGGCTTTGACTATTACCAGACACTCTTGATAAGCAGTA
ACAGCAGTAAGAAGAGACCGAAGGATTCTTCTTTGTTATCGGAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAGATGTCTTATCTTATCTTTCTTATCTTAAAGACCTACCATTTGTTC
CTTTTCTATTTTGGCAGCCCGGGTATTCGCAAAGGGAAAAAACCCAAGACAGCATTCCT
TGTTCATTATGACTATTACAAAGCCAGGAATGATTTCGATGGCCGACATGAATTACGTCG
TTTCCAAGAACAGAAGCTTAAACCGTCCTGCTGAGCGGGGCGGTAATCGGTGA

>YNL143C, 130 aa (SEQ ID NO 334)
MREQLKLFTREIVDFTFLILSGFDYYQTLLISSNSSKKRPKDSSLLSEKKKKKKKKKDV
LSYLSYLKDLPFVPFLFWQPGYSQREKNPRQHSLFIMTITKPGMISMADMNYVVSKNRSL
NRPAERGGNR

>YNL179C, 938 bp, CDS: 501-938 (SEQ ID NO 335)
ACAGCGGTTAATTTCAAATACCCTAATCGGAGGTCTTATCTTATTTTTCAAGGGCAAGGC
TCTCCACATCGGTAAGTGATGACCAGATAATGGAAAGTAGCAGAATTTTATTTATGTGCC
ATACAAGCCCGGAGAAACAGAGTAGCTAAAAAATTAAGGTGTGCAAAAGTGGTTTTGTTC
CCCGACGCCCGGGCCTTTCTCTCCCCTGAATCTTTTCGTTCCGGCCCCCTCTCTCAATA
CCAGATCTGCATCTATACTAAAGCTGCAGTGAGAGTAAACCGGAAAATTATCCTGCGTGT
TTGCTTCGGTCTTAGCTTTTACTTGGGTATGCGAGAACCTCTAAGAGCTTAGACCGGTCT
TCCTCCCTAAAAAGAAAATTATAAAAGGTTATTATCTGGACTAAAGCAAAAAAAAAACAA
CGTTTCGGCGTCCGCTCAAAATTTTCATTACGCTTCTTGGTCAAATCAGTTACGTAACGG
GTTATGACGAATACGATGAGATGAGTAATTGCAGAAGGCTCCTATGCAGACAGCTAAGCA
GTGCTTACTTGAATTACCTTCCCTTTTATTTCTTGATATATCGTCCTTTTTCTCTCTATC
TTAGTTCTTGCGAGTACTGGCAATCATGTTTCTCCTTTTTTTTTCTTTTTTTTTATTTT
TTTTTTTTTTTTTTACTTTTCAGTTTCTCGTAGCTTTTCCTATTTTGCTATTTAAAGTAA
GTTTAAATAGTACCCTCACTAAACACGTACGGCCGATCCACCAACGAACAAAAGCACGAT
CCTTGACCCATCATTGTATTCCAAAGCGTTGGAACATTCACTTTTTTTTTTCCGGTCTAT
TGCACAAGACAATATCCAGAATATTCAGTTGGATAGGAAATACAAGACAGGTGGCACCCA
CAAAGCACACGCCGAAATATTTATTAAATACAATATAG

>YNL179C, 145 aa (SEQ ID NO 336)
MSNCRRLLCRQLSSAYLNYLPFYFLIYRPFSLYLSSCEYWQSCFSFFFLFFLFFFFFFTF
QFLVAFPILLFKVSLNSTLTKHVRPIHQRTKARSLTHHCIPKRWNIHFFFSGLLHKTISR
IFSWIGNTRQVAPTKHTPKYLLNTI

>YOL150C, 812 bp, CDS: 501-812 (SEQ ID NO 349)
TTCCCATTTCCACTGCTATTCCTGTTGCTATTGTCAGAACCATTGTTTACTTGAATGTTA
TTACTACCATTTTGTGAATCAAAAATATCTACTTCTTGTGGGGAGACGGGTAGAAGATTT
GTATTTTGCGAGACGTCTCTCAAATATATGGCCAAAACACCTTGATATTCTAGTTTATTC
CATTCGTCCTTCTTGAAGTCCCATTTATACAGTGACGCATGTGGTGTGTGAAAAAGTAGT
TGCTTTATTTTTGGATCGTATCTCCCAATAACGTTGAAATTCAAAGCTTTTCTATAGAAT
TCTAACTGTGTGGCAGAGTTTTCTGCTGCAGTTGCTGCTCCGGTCATTGTGCACAGCTTT
TCTTGTGATGTGTTGCAAAGATAAATGCTTATCTGAACGTTTCTCTATTGTTTTTTCGTC
AATTTTCTTTTCTTTCTTGCTTCGCGTTTTCGACATATTAAGCTGTATATAGAAGAGAAA
AATGCGCAGAGATGTACTAGATGATAAAAAATAATTGTAATAACGTTAATATATATAAAT
ATTATCTATTTTCATTTAAAGTTTATATTCTGCCCTCAAATTTTAAAATTTGGGAGGCAG
TGTCGTCAATGGTCTCTTTCAAGTTCCTGAACTTGAAACCTAACAATTTCTTACTCTTTT
TATTATCAAGAGTAGCACCAAGGGTGTTATGGGTAGCACCAGAACCTGGTTTCCCCACTG
GAATATTGCCTTTTAGAACAGGGAAGTCTTCGTTAAGGATATCGAGAACATCCTGCATAG
TAAATCTGGCCTCCGATACGATTAGTCTTTGA

>YOL150C, 103 aa (SEQ ID NO 350)
MIKNNCNNVNIYKYYLFSFKVYILPSNFKIWEAVSSMVSFKFLNLKPNNFLLFLLSRVAP
RVLWVAPEPGFPTGILPFRTGKSSLRISRTSCIVNLASDTISL

>YOL151W, 1529 bp, CDS: 501-1529 (SEQ ID NO 351)
GCGTGAACTATGTCATATTTGCGATTTAGGTACAATAAATTATTATCATTATTATATTAT
GTTTGCATGTAGGTTCTACAAATACATTGTTGTACGCTATAGTTTCCTTTCAAAACTAGA
AAGAATTCGTAACAAAATAATCTCCAATATTTTATAGCACCTTATTAATATCAATGCTGC
AATACCTTCTCATTTCAACAATTGGCCCTCACCTCTTTTGTACAAAAAACGTCGCCATTG
ATAAAATAAGTAAGAAGCATATAATTGGAATGTCCATTACGTAAAAGAAAAAAAATCATG
TGTACATATTACGTAATAGAATACGGAATTTTCTCGCGGAAGTAGATCTTCCGTGGAAAA
AAAGGAAAAAGTCCGATCAATATTGAAAAAGGGATCCTTAGTTTCCCAACTATATAAGGA
GGAAAAGTCTATCTCTGTAGCGTTGATATAACGTGTACGATTTTCAAACAAACAGATAGC
AGTATCACACGCCGTAAATATGTCAGTTTTCGTTTCAGGTGCTAACGGGTTCATTGCCC
AACACATTGTCGATCTCCTGTTGAAGGAAGACTATAAGGTCATCGGTTCTGCCAGAAGTC
AAGAAAAGGCCGAGAATTTAACGGAGGCCTTTGGTAACAACCCAAAATTCTCCATGGAAG
TTGTCCCAGACATATCTAAGCTGGACGCATTTGACCATGTTTCCAAAAGCACGGCAAGG
ATATCAAGATAGTTCTACATACGGCCTCTCCATTCTGCTTTGATATCACTGACAGTGAAC
GCGATTTATTAATTCCTGCTGTGAACGGTGTTAAGGGAATTCTCCACTCAATTAAAAAAT
ACGCCGCTGATTCTGTAGAACGTGTAGTTCTCACCTCTTCTTATGCAGCTGTGTTCGATA
TGGCAAAAGAAAACGATAAGTCTTTAACATTTAACGAAGAATCCTGGAACCCAGCTACCT
GGGAGAGTTGCCAAAGTGACCCAGTTAACGCCTACTGTGGTTCTAAGAAGTTTGCTGAAA
AAGCAGCTTGGGAATTTCTAGAGGAGAATAGAGACTCTGTAAAATTCGAATTAACTGCCG
TTAACCCAGTTTACGTTTTTGGTCCGCAAATGTTTGACAAAGATGTGAAAAAACACTTGA
ACACATCTTGCGAACTCGTCAACAGCTTGATGCATTTATCACCAGAGGACAAGATACCGG
AACTATTTGGTGGATACATTGATGTTCGTGATGTTGCAAAGGCTCATTTAGTTGCCTTCC
AAAAGAGGGAAACAATTGGTCAAAGACTAATCGTATCGGAGGCCAGATTTACTATGCAGG
ATGTTCTCGATATCCTTAACGAAGACTTCCCTGTTCTAAAAGGCAATATTCCAGTGGGGA
AACCAGGTTCTGGTGCTACCCATAACACCCTTGGTGCTACTCTTGATAATAAAAAGAGTA
AGAAATTGTTAGGTTTCAAGTTCAGGAACTTGAAAGAGACCATTGACGACACTGCCTCCC
AAATTTTAAAATTTGAGGGCAGAATATAA

>YOL151W, 342 aa (SEQ ID NO 352)
MSVFVSGANGFIAQHIVDLLLKEDYKVIGSARSQEKAENLTEAFGNNPKFSMEVVPDISK
LDAFDHVFQKHGKDIKIVLHTASPFCFDITDSERDLLIPAVNGVKGILHSIKKYAADSVE

RVVLTSSYAAVFDMAKENDKSLTFNEESWNPATWESCQSDPVNAYCGSKKFAEKAAWEFL
EENRDSVKFELTAVNPVYVFGPQMFDKDVKKHLNTSCELVNSLMHLSPEDKIPELFGGYI
DVRDVAKAHLVAFQKRETIGQRLIVSEARFTMQDVLDILNEDFPVLKGNIPVGKPGSGAT
HNTLGATLDNKKSKKLLGFKFRNLKETIDDTASQILKFEGRI

>YOR131C, 1157 bp, CDS: 501-1157 (SEQ ID NO 359)
TCCTGAACGGAAGCTGCAGTTTGCTCAGTACCTACACGCTCCTCTGACATAGAAGATGAT
CCATCTGTGGTTGTTGCAGCAGGTTCAGAATCTTCCTCCTGGGGCTCAGCAAATGGATTG
TTATCCAGATCATCATATGGATCATAAGGTACAGCCGAAGTCATTGTTCAGAGGATAGAT
GGATTGACTAAGGGTACAGTACGGCAAAAAAAAATTAGATCAGCTTTTCAAAACAAACTA
TTTTGGCGTTTACCAAAACCAAAACAGTATATTCAACTAGTTCAATCACTCTTGAAAACG
TCCCCTTTCTACAAAATTAGGCTTTGAACGCGTGCTATGGAAAAAAGTGTAAAGAAAACG
AAAAAACCAGAAAAGTCATATATATCTTATAACGAAATATCAGGGTGTTCGACTCAATCG
CCAGGTGCCGCTAACACAATCATTAGGATAGTCGGGCAATATATACGGTTCAATAGTCAC
TGAAAGTGTATCACAGAATAATGACAAAGCTACAAGGACTACAGGGATTAAAACACATCA
AAGCGGTTGTATTTGATATGGATGGCACATTATGCCTACCCCAGCCTTGGATGTTTCCAG
CAATGAGAAACGCCATAGGATTGGAGGACAAATCGATTGATATCCTTCATTTCATTGATA
CATTGCCCACAGAAAAAGAAAAAAAAGAAGCGCATGATAGAATAGAATTAGTTGAGGCAA
AAGCCATGAAGGAGATGCAACCGCAGCCTGGTCTGGTTGACATAATGAGGTATTTGACGA
AAAATGGTATTAGCAAGAACATATGTACTAGAAATGTCGGAGCCCCGGTAGAGACTTTTG
TTAAAAGATTTATTCCATCCGAGCTTTCGAGGTTTGACTATATTGTGACAAGGGAGTTTA
GGCCTACAAAACCGCAACCAGACCCATTATTACACATCGCCTCGAAGCTAAATATAAGGC
CCTTGGAAATGATCATGGTAGGAGATTCATTTGACGACATGAAATCCGGTAGATCTGCTG
GATGTTTCACGGTATTACTCAAGAATCATGTGAATGGACATTTACTGCTCGAACATAAAG
AACTAGTAGACGTTTCAGTAGAGGATCTTTCCGAAATAATTGAATTGATTCAAAATATGA
ATAAAGAAAGTTTCTAA

>YOR131C, 218 aa (SEQ ID NO 360)
MTKLQGLQGLKHIKAVVFDMDGTLCLPQPWMFPAMRNAIGLEDKSIDILHFIDTLPTEKE
KKEAHDRIELVEAKAMKEMQPQPGLVDIMRYLTKNGISKNICTRNVGAPVETFVKRFIPS
ELSRFDVIVTREFRPTKPQPDPLLHIASKLNIRPLEMIMVGDSFDDMKSGRSAGCFTVLL
KNHVNGHLLLEHKELVDVSVEDLSEIIELIQNMNKESF

>YOR286W, 950 bp, CDS: 501-950 (SEQ ID NO 367)
CATCTGAGTACTCGATTGTTCATATTCCTGCTTCCATCAATGTGCCATATAGATCGCACC
CTGACGCATTTGCCTTAGATCCTTTAGAATTTGAGAAACAGATTGGCATCCCAAAACCTG
ACAGTGCCAAGGAGCTAATATTTTATTGTGCTTCTGGCAAACGCGGGGGAGAAGCTCAAA
AAGTCGCCTCCTCACATGGATATTCAAACACCTCACTATATCCTGGCTCTATGAATGATT
GGGTTTCTCATGGGGGTGATAAACTTGACTTATAGCCTTGTATACTCTAGGTATGTACCC
TGTGTATTTTCGTAAGCTAGTAACGTATTATGCCATTTATGTCACACCGTTCATAATATT
TGCCTATTGCATTGGCTGTGATAGCGGCGGCGCAAAGAAATTAGGAAGTATAAAAAAAAA
AATACAAAACTTAATCTGAATGGAATAAGATAGCGATAACTCTCAACAAATGGAAGCGAG
ACAGAAGAAAAAGACCAACGATGTTCAAGCATAGTACAGGTATTCTCTCGAGGACAGTTT
CTGCAAGATCGCCTACATTGGTCCTGAGAACATTTACAACGAAGGCTCCAAAGATCTATA
CTTTTGACCAGGTCAGGAACCTAGTCGAACACCCCAATGATAAAAAACTATTGGTAGATG
TAAGGGAACCCAAGGAAGTAAAGGATTACAAGATGCCAACTACAATAAATATTCCGGTGA
ATAGTGCCCCTGGCGCTCTTGGATTGCCCGAAAAGGAGTTTCACAAAGTTTTCCAATTTG
CTAAACCACCTCACGATAAAGAATTGATTTTTCTTTGTGCGAAAGGAGTAAGAGCCAAAA
CTGCCGAAGAGTTGGCTCGATCTTATGGGTACGAAAACACTGGTATCTATCCTGGTTCTA
TTACTGAGTGGTTAGCTAAAGGTGGTGCTGACGTTAAGCCCAAAAAATAA

>YOR286W, 149 aa (SEQ ID NO 368)
MFKHSTGILSRTVSARSPTLVLRTFTTKAPKIYTFDQVRNLVEHPNDKKLLVDVREPKEV
KDYKMPTTINIPVNSAPGALGLPEKEPHKVFQFAKPPHDKELIPLCAKGVRAKTAEELAR
SYGYENTGIYPGSITEWLAKGGADVKPKK

>YOR382W, 962 bp, CDS: 501-962 (SEQ ID NO 375)
AGTAAGCTCCTACAGTGAAATATCTGGGTGCTACTGACGCCAAGCCCTACAGCGATCGGA
ATGCGGGAACGGAAGTTAACGGGGCTTCCAGAACGGCGGAAGCGAATTGAACGAGGACGG
CAAACAAAAACACCCAAAATTTCATTACTTAGAATGACCCTCAAGAGCAGGGTGCAATTTT
ATCAAGCGATCATTGAACTAACTAAGTTCATATCCTGTATAGGATTTAAAACAATGCACC
CTAAGTTCAAATGCACCCCCCCTCGCCCCGCAGCCGGACCCTTGAACAGAGAACTGTTTCG
AGGTTCACCCAATTGGATCACTTGTATAATTTGTAATCGAGTTCGGATAAGATGTATACG
AATCTAACTGGGTGCAGTATAATTAGCATTTTATATTACCTAGCAATATATGTATAAAAC
AGGAATGTGTGCGTGCTTCAGGCAGAATTTTACGGTCCTTGTAAAAAAGTCTATCATAAA
GCCATCACAAAACAATAATAATGAAATTCTCAACTATTTTCGGAGCTACTACAGTTATGA
CTGCCGTCTCGGCAGCAGCTGTGTCGAGTGTAATGACCACTAAGACTATTACTGCTACTA
ACGGTAATAACGTTTACACTAAGGTCGTTACCGACACCGCTGACCCTATCATTAGTTACA
GTACCACTAGAACTGTCGTTGTCAGTAATAGTGATGCTACTTACACAAAGGTTGTCACCG
AAGGACCAGATACCACCTCTGAAAAGAGTACAACAAAGACACTTACTTTGACAAACGGTT
CAGGTTCATCAACCAACCTTTACACCAAGACCGTCACTCAAGCCGTCGAATCATCTACAT
CCTCCTCATCCTCCTCATCCTCCTCCTCCTTCTCGCCTCTTCTTCTGGTGCTGCTCCTG
CTGCATTCCAAGGAGCAAGTGTCGGTGCATTGGCCCTTGGTTTGATTTCTTACCTATTAT
AA

>YOR382W, 153 aa (SEQ ID NO 376)
MKFSTIFGATTVMTAVSAAAVSSVMTTKTITATNGNNVYTKVVTDTADPIISYSTTRTVV
VSNSDATYTKVVTEGPDTTSEKSTTKTL/TLTNGSGSSTNLYTKTVTQAVESSTSSSSSS
SSSSSASSSGAAPAAFQGASVGALALGLISYLL

>YPL078C, 1235 bp, CDS: 501-1235 (SEQ ID NO 379)
TAAACTGTGTTGTGACGCAACTGCAACTCCCAGATGAAATACGGTCCGGTAAAGATAGGA
ATATTCTACTCTACAAGCATGAATATTTTTTAACGCGGCGCAGTACTATACAGCATAACA
GGTCTTCCACGCATGAGAAACTGTCCATGGCTAAATTAGTTCCTCACACAGAATTAGAAA
TGTGCTGTGACAATGGCACATACGTAGATAAAAGATAAATATAATTCAGAATGGCTGTGG
CGACAACTATTATCATAGAGGTGTCCCATCGAGCGAGCCTCATTGGCCGGGTAATCGACA
TCAATATTGAACCAATCACGACGCTTTTTCTCTTCACCGCTCATTCGGACCTTCACCACA
GGTTTGGGTAATTAAAATAGCAAGGGATTATAATTGCAGTTAGCAGTTTATGTTGACAAG
TTTATACTGTGCTAGGAAGGGTTATATTTTATTAAAAGACTGACGAGAATTCAGTACCTC
CTAAGTGCGCAAGAGATAAAATGAGCATGAGTATGGGTGTCCGTGGCCTAGCGTTAAGGT
CCGTTTCTAAAACATTATTTAGCCAAGGTGTTCGTTGTCCTTCGATGGTGATTGGAGCCC
GTTATATGTCTTCCACTCCAGAAAAACAGACAGATCCAAAAGCAAAGGCTAACTCTATCA
TCAATGCCATTCCAGGTAATAATATTTTGACAAAGACGGGGGTTTTGGGGACTTCTGCTG
CCGCTGTCATTTATGCCATTTCCAATGAATTGTACGTTATCAACGATGAAAGTATTTTAT
TGCTGACTTTTTTGGGTTTCACTGGTTTAGTGGCAAAGTATTTGGCGCCAGCATATAAAG
ATTTTGCCGATGCAAGAATGAAGAAAGTCTCCGACGTTTTAAATGCCTCGAGAAACAAGC
ATGTCGAAGCTGTTAAAGATAGAATCGACTCTGTCTCTCAACTACAAAATGTTGCTGAAA
CTACAAAGGTTTTGTTTGATGTTTCCAAGGAAACTGTTGAACTTGAAAGCGAAGCCTTTG
AATTGAAACAAAAGGTAGAATTAGCTCACGAAGCAAAGGCAGTCTTAGATTCGTGGGTTA
GATATGAAGCTTCCTTGCGTCAATTGGAACAAAGGCAACTAGCAAAATCTGTCATCTCCA
GAGTTCAGTCAGAATTGGGTAATCCAAAATTCCAAGAGAAAGTTTTGCAACAGTCTATAT
CTGAAATTGAACAATTGCTTTCTAAATTGAAGTAA

>YPL078C, 244 aa (SEQ ID NO 380)
MSMSMGVRGLALRSVSKTLFSQGVRCPSMVIGARYMSSTPEKQTDPKAKANSIINAIPGN
NILTKTGVLGTSAAAVIYAISNELYVINDESILLLTFLGFTGLVAKYLAPAYKDFADARM
KKVSDVLNASRNKHVEAVKDRIDSVSQLQNVAETTKVLFDVSKETVELESEAFELKQKVE
LAHEAKAVLDSWVRYEASLRQLEQRQLAKSVISRVQSELGNPKFQEKVLQQSISEIEQLL
SKLK

>YPL085W, 7088 bp, CDS: 501-7088 (SEQ ID NO 383)
TTTTTCATGAGGAAGAGCCAGTGACAGTAAATAATAAAAGGTGAAATGATTAAACAATGA

AAGCGGCAGAAAAATAAAATCAAACAGTGGCAGTATTGACTTTTGAAAATCAGAAGTTCA
TCCTAAGTTAAGACTTTCTTCTTTTAAGTGCTTTCTCCTTCTCTCACTGTCTTTATCGCTG
TATATCTCATTGTTGAATAATATAACACAACGTTATAAGTGATCATCACTTTCTGATCCA
TAATTTCAAACCTCAAGCGACCGTACATGTGGCATTTTCCACTATAAACTTACGAGCAAG
AGAAAGATATACGGAAAAGGTTAATTGGCAGGTTACACAAGATTTTGGTCATTGAATATT
TGCAGCCCTCCTGCTTGAGAAACTGGACAACAACTGTTATCAATATTCCCTTTTCAAAAT
AGTGGTATTTAACTGGCCATAACCAAGGAAACCGTTGTACCTATTATTTTGTATAGTCTT
CATTTAATAACGTGTTAAGAATGACACCTGAAGCCAAGAAAAGGAAAAACCAAAAGAAGA
AGTTGAAGCAAAAGCAAAAAAAAGCTGCTGAGAAAGCTGCTAGCCACAGTGAAGAACCAC
TTGAATTACCAGAAAGTACGATTAACAGCAGCTTCAACGACGACTCGGTGAACCGTACAG
AATCTGACATAGCTTCAAAATCTGATGTTCCTCCGGTCTCATCATCTACCAATATCTCTC
CGGCTAATGAAACACAACTAGAAATACCTGATACTCAAGAATTGCATCATAAACTGCTCA
ACGACTCTGATCAACATGATATTACCGCGGACTCAAATGATTTGCCAGACAACTCAATCG
TTGAACATGACTCTGTTATTACCCAAACAAAACCAGCCATGTCTCAAGAATACGAAGAGA
CTGCCGCTCACTTATCTTCGAGAAATCCATCGCTCGATGTAGTCGCGGGAGAACTTCACA
ATAATAATGAACATACCCAGAAAATTGCCGTATCCGCTGTGGAAGAGGATTCTTTCAATG
AAGAAGAGGGTGAAAATCACGACAGCATAATAATTTCATCATTAAACGATGCTACCCCTT
CTCAATATAATCATTTTCTCCCATCCGATGGCAATCTTCTTTCTCCAGAATTATCTTCTG
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AGTATTGTAATGATGAAGGAAATTAGTTTGAACGCAAATAATGTGCTTCCTGATGAACTTT
CAAAGGAAGAAGATGAAAGATTAAAACTAGAAACGCATGTATCAACCGAAGAAAGAAAC
AGGATATCGCTGATCAGGAAACTGCAGAAAACTTATTTACGTCTAGTACAGAACCATCTG
AGAATAAAATAAGAAATTCTGGTGATGATACCTCCATGTTGTTTCAAGATGACGAAAGTG
ATCAGAAGGTTCCATGGGAGGAAGATGTGAAGAAAGATTTTCATAATGAGAACACAAATA
ATACTCAAGAATCGGCACCGAACACAGATGATCGTGATAAGGGTTATGAAGGAAACGAAG
CTTTGAAAAAGTCCGAAAGTTGTACAGCCGCGGACGAGAGGTCGTACTCTGAAGAAACTT
CAGAAGATATCTTTCACGGACACGACAAACAGGTAGTTGAAGGCCAAAATGATTTCACTG
GGAAAAATATTGAGAATGAAAGCCAGAAATTAATGGGGGAAGGGAATCATAAGTTACCGT
TGTCTGCCGAAGCTGACATTATAGAACCTGGTAAGGATATTCAAGATCAAGCCGAGGATT
TGTTTACGCAGAGCAGCGGAGACTTGGGAGAAGTTTTGCCATGGGAATCTACTGATAAAA
ACGCTGATGTAACGAGCAAATCCCAAGAGAAACATGAAGATTTATTGCTGCTTCTGGAA
ACGATGAGAAACTTCCTTGGGAAGTTTCTGACGGTGAAGTATCATCGGGAAAGACGGAAA
ACAGCATGCAGACTAGTACTGAGAAAATAGCTGAGCAAAAGTTTTCGTTTTTGGAAAACG
ACGACGACCTTTTGGACGACGACGACAGCTTTTTGGCTTCTTCTGAGGAAGAAGACACAG
TACCTAATACCGATAATACAACGAATTTAACCTCAAAACCAGTTGAAGAAAAAAGGCTT
CAAGATATAAACCTATTATCGAGGAGGAAGCAGGAATGCGTCAAGAGCAAGTTCATTTTA
CCAATACTACTGGCATTGTAACACCGCAGCAGTTCCACGGTTTGACTAAAACTGGACTAG
GCACCCCCAACCAACAAGTCAGTGTACCAAATATAGTTAGTCCTAAGCCTCCTGTGGTAA
AAGACAATCGTTCAAATTTTAAGATAAATGAGGAGAAAAAGAAGTCTGATGCTTACGATT
TTCCACTGGAAATTATTTCAGAAAGTTCCAAGAAGGGTCACGCAAAGCCGGTTGCCGTTC
CTACTCAAAGGTTTGGCTCAGGGAATTCTTTTAGTTCTTTGGACAAACCAATTCCACAGA
GCAGGAAAGGCTCTAATAACTCAAATAGGCCACCCGTGATCCCATTGGGGACGCAGGAGC
CTCGATCTTCGAGAACTAACTCAGCGATCTCGCAATCTCCCGTTAATTATGCTTTCCCTA
ACCCATACAAAATTCAACAACTACAACAGGCTCCTATCCAATCAGGTATGCCTTTACCAA
ATACCAACATACCTCCCCCAGCATTAAAAGTGGAAACCACCGTTTCTGCTCCTCCAATTC
GGGCAAGAGGGGTCAGCAATGCCTCCGTGGGAAGTTCAGCGTCTTTTGGTGCTAGACATG
CAACACAGTACGGCCTCAATAACGGGGTACCTCCGGTTTCGCCATATGGTCAAGCTACCA
TAAATTTGCCAACTGCCGAATAAGTATGCCCCCGTCTCTCCTACAGTTCAGCAGAAGCAAT
ATCCATCAGTTGTGCAAAACCTTGGCGCTTCGGCCGTAAATACCCCCAATTTTGTAAAGA
CCCATAGAGGCCATACAAGCTCTATTAGTTCGTATACACCAAACCAGAATGAACACGCCT
CTAGATACGCACCCAACTATCAACAATCTTATCAGGTGCCATATACCTCACAACCTGTTG
GTCCTGTAGCTGGGAATTCAAGCTATCAAAGCCAAACCCGAAGTTCTTATGCAGTTCCTA
TGATGCCCCAGGCTCAAACTTCAGCAAGTATTCAGCCTCACGCGAACATTCAACCGCCTA
CTGGCATTTTACCTTTAGCCCCCTTACGACCTCTAGACCCCTTACAAGCCGCTACGAACT
TGCAACCCCGTGCAAGCAACATAACGGCTGCAAATTCACTACCTCTTGCAAATTTGCCAC
TTGCTGAAAACATACTGCCAGAAATTATCACGCATCGAGCTACAAGTAGTGTTGCACCAC

CACGACAGGAAAATAATCCAATTAAAATAGACAACGAGGCTTTATTACGCCGTCAATTTC
CGATTTTTCATTGGAGTGCTGCAAACAAGGTCGTGTACGCAGTCCCCCCTATCCCTGACC
AATCGCAGTACATGATTTCATCAAGCATTGTACAGGAAATAAAAGTGACACCAATTGACC
AGATAATTAAACCGAACGATATGCTCAAAAGCTTCCCAGGTCCTTTGGGTAGTGCCAAAT
TAAAAAAAAAGGATTTAACCAAATGGATGGAAACCACTATTAAATCCATATCTGAAAATG
AATCATCCACTGATATGACTATATGGCAACTATTGGAAATGAAACTAAACGATAAAGTTA
ACTGGAAAAATATTTCAAAACTACTATACAATTCTGACGAACTTTTAATGTACCTATCTC
AGCCCTTTCCAAACGGTGACATGATTCCAAATGCATATAGACTGGATATAAATTGTCAGA
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TACAATAA

>YPL085W, 2195 aa (SEQ ID NO 384)
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>YPL190C, 2909 bp, CDS: 501-2909 (SEQ ID NO 387)
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>YPL190C, 802 aa (SEQ ID NO 388)
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DDDDDDEEEEEEEEEEGNDNSSVGSDSAAEDGEDEEDKKDTKDKEVELFNERFDGTGL
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DDAVAIFNNIKNNRNNSRPTDYRAMSHQQNIYGAPPLPVPNGPAVGPPPQTNYYQGYSMP
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>YPL201C, 1886 bp, CDS: 501-1886 (SEQ ID NO 389)
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>YPL201C, 461 aa (SEQ ID NO 390)
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GEDGGDVGNYSEEDDDGDEEKELEDVFRSNRGLEFVRINNYFTTHDLQSFKSFRNFNSKY
WIFYSNQAEDKKLLLYDFNGQHLIFIKQQFYGQLNLLLSDAIICMDCNFGYNSNTIQILV
GFQNGKLLKLNCDLNGNVNNHLLLKDPSTSSHQSHLSILNVWAGLLPHFVVSFSLKDGLL
ITSLDHQQSNGSFQSFHTNIDLPVDLRTTTNVKSVLNFPQFTLYKGNDMIFHCKNLLGSD
ASTLNKEINFMLKIDEDVQKIDYLLKTNHILLETNMRYLSIPTRDPIENSNSSPPVSDSE
VYPIFYKTQELHVHASGTGRQIANNGKYIFITEQHLYGTALSVYKYSISFKRWLFVGYSD
IRAKYGIRSVKDLFVGNCPSVNSPVLTILTDDNNIQTILLK

>YPR028W, 1176 bp, exon1: 501-551, intron1: 552-684, exon2: 685-1176 (SEQ ID NO 393)
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>YPR028W, 180 aa (SEQ ID NO 394)
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KTVFLIYIALPQTGGARMIYQKIVAPLTDRYILRDVSKTEKDEIRASVNEASKATGASVH

YDR145W, 2120 bp, CDS: 501-2120 (SEQ ID NO 99)
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CTGAAATTTCAACTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAACGATGTGTATGAATCCCGTCTTAATTAGTAAATAGGGTCTAGTAAG
CGTAGCGAGGATGAATTAAATGCATTGTTGAATATGAAGAGCACCTTATG
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GAAGACAACAGGCTGCGCAAGCCTACAATAATACTTCAAATTCAAATTCA
AGCAATCCAGCTTCTATTCCTACTGAAAATGTCCCTAATTCATCACAGCA
ACAACAACAACAACAACAACAGACAAGAAACAACAGTAACAAATTTAGCA
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GCTTGAATACAAAAAATAA

YDR145W, 539 aa (SEQ ID NO 100)
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SNPASIPTENVPNSSQQQQQQQQQTRNNSNKFSNMIKQVLTPEENQEYEK
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TTKLPPYEMDTQRVMSKRKLRELVKTVGIDEGDGETVIDGDVEELLLDLA
DDFVTNVTAFSCRLAKHRKSDNLEARDIQLHLERNWNIRIPGYSADEIRS
TRKWNPSQNYNQKLQSITSDKVAAAKNNGNNVASLNTKK

YDR216W, 4472bp, CDS: 501-4472 (SEQ ID NO 109)
CAAAGAACAACGCCTTAAAAATAGGAAAACGTTTCGCTACAGGTGTTGT
TATTATTGTTGTTGTGCTGTTGTTTATTGTGCTATACTTGTGGTATTTAT
TCTGGACTTCCGATCGGAAATTTTCTTCCCTTGAAGACCTTTGAAGACA
ACAGTTATATATCATTGATCTGAATTTCTCAGGCTATTTTCAAAATTCCA
TACCTCCTTATTCCAACATTTGCTCGACTACTATAGAAAAGCCTTATTCT
TTTATCTTTGAAAGAAAGAAAAGGTGTCATAGCAAAAGTTTATTGTTACT
CTGTTTTGATATACTCCCTCTTATTCGTTGGAAGTATAAGATTGATTTGC
ATAAATTAACCAATCATTTTGCTACTTTCCCGGTTCTCCCTTTATTATAA
ACACTTCAGAAAAATATTCTGCTACTATTCCTTACTTTACTATAAGAATT
TTGTTTTCCAAAAAAAAAAATATAAAAAAAATAATCATACTCTATTACT
ATGGCTAACGTAGAAAAACCAAACGATTGTTCAGGCTTTCCCGTTGTTGA
CTTGAATTCGTGCTTTTCTAACGGCTTCAATAATGAGAAACAAGAAATAG
AAATGGAAACGGATGATTCACCGATTTTATTAATGTCATCATCAGCTTCC
AGAGAAAACTCAAACACTTTCTCTGTGATACAGAGGACGCCAGATGGAAA
GATCATTACCACAAATAATAATATGAACTCCAAGATTAACAAGCAACTGG
ACAAGTTGCCCGAAAATTTAAGGCTTAATGGTAGAACCCCCAGTGGGAAA
CTAAGGTCATTTGTTTGCGAGGTTTGTACGAGAGCGTTCGCAAGACAAGA
GCACTTGAAAAGACATTACAGATCGCATACAAATGAAAAACCTTATCCCT
GTGGCCTCTGCAACAGATGCTTTACTAGGAGGGACTTACTGATCAGGCAT
GCTCAAAAAATCCATAGTGGTAATTTAGGGGAAACGATTTCCCATACCAA
GAAAGTGTCGAGAACTATAACTAAAGCTCGGAAAAATTCTGCATCCTCAG
TCAAGTTTCAAACTCCAACCTATGGTACTCCAGATAATGGTAATTTTTTG
AATCGCACTACTGCCAATACAAGAAGAAAAGCAAGCCCTGAAGCTAATGT
TAAACGTAAGTACTTGAAAAAACTGACGCGCAGGGCTTACTGATCAGCAC
AATCAGCATCCAGCTATGCTTTGCCCGACCAATCTTCGCTAGAACAACAT
CCAAAGGATCGTGTTAAATTTTCTACGCCTGAATTAGTTCCACTTGACTT
GAAGAATCCTGAACTTGACTCTTCGTTTGACCTGAATATGAATCTAGATT
TAAACCTAAATCTAGATTCCAATTTCAATATAGCATTAAACCGTTCTGAT
TCTTCTGGATCAACAATGAATTTGGATTATAAATTGCCCGAATCAGCAAA
TAACTACACATATTCTTCCGGCTCACCAACCCGCGCATATGTCGGCGCTA
ACACGAATTCTAAGAACGCTTCATTTAATGACGCAGACTTATTGTCGTCG
TCGTACTGGATAAAAGCCTATAATGATCATTTGTTTTCAGTATCTGAAAG
TGATGAAACTTCTCCAATGAACTCTGAATTAAACGACACTAAATTAATCG
TCCCAGATTTTAAATCGACTATACATCATTTGAAGGATTCAAGGTCCTCC
TCTTGGACTGTTGCTATAGATAATAATAGCAATAACAATAAGGTATCAGA
CAACCAACCTGATTTCGTCGATTTTCAAGAACTGCTGGATAATGATACTT
TAGGTAATGATTTGTTAGAGACCACTGCCGTTTTAAAAGAATTTGAACTT

TTACATGATGATAGCGTAAGTGCTACCGCCACGTCAAATGAGATTGACCT
TTCCCATTTGAACCTATCAAACTCTCCAATTTCTCCTCATAAGTTAATTT
ATAAGAATAAAGAGGGGACCAATGACGATATGTTGATTTCTTTCGGACTC
GATCATCCTTCCAATCGCGAAGATGATCTGGATAAGCTATGTAATATGAC
CAGAGATGTTCAAGCCATATTCAGTCAATATTTGAAAGGAGAAGAGTCTA
AACGATCCCTGGAAGACTTTTTATCAACGTCAAACAGGAAAGAAAAGCCA
GATAGCGGCAACTATACTTTTTATGGGTTAGATTGTTTAACGTTATCGAA
AATATCAAGAGCTCTGCCGGCCTCCACTGTGAACAACAATCAGCCATCGC
ATTCCATAGAATCAAAGCTATTTAATGAACCAATGAGAAATATGTGCATT
AAAGTGCTTAGATACTATGAAAAGTTCAGTCATGATAGTAGTGAGAGTGT
CATGGACTCTAATCCAAACTTGCTGTCCAAAGAATTGTTAATGCCAGCTG
TGAGTGAATTGAACGAATATTTAGATCTTTTCAAGAATAATTTCCTTCCC
CATTTCCCTATTATTCACCCAAGCTTGCTTGATTTGGATTTGGATAGCTT
GCAACGATATACTAATGAGGATGGGTATGATGACGCTGAAAACGCGCAGT
TGTTTGATCGATTAAGTCAAGGGACAGATAAAGAATATGATTACGAGCAC
TATCAAATCTTGTCCATTTCGAAAATCGTTTGTTTACCCTTATTTATGGC
CACATTTGGTTCTTTGCATAAGTTCGGTTACAAATCTCAAACAATAGAAT
TGTATGAGATGAGTAGAAGAATTCTACATTCTTTTTTGGAGACTAAAAGA
AGGTGTCGCAGTACAACAGTAAATGACAGTTATCAGAACATTTGGTTGAT
GCAATCCCTAATATTGAGCTTCATGTTCGCTCTAGTTGCTGATTATTTGG
AGAAAATTGACTCCTCTTTGATGAAAAGGCAATTGTCCGCATTATGTTCA
ACGATCAGATCAAACTGTTTACCGACAATTTCTGCAAATTCTGAGAAGAG
TATCAATAATAACAATGAACCTTTAACATTTGGTTCTCCTCTTCAATACA
TCATTTTTGAGTCAAAAATTAGATGCACCTTAATGGCTTATGATTTTTGT
CAGTTCTTGAAATGTTTCTTCCATATTAAATTCGATTTGTCTATAAAGGA
AAAAGATGTTGAAACCATTTATATTCCCGACAATGAGTCAAAATGGGCCA
GTGAATCGATAATATGTAATGGGCATGTTGTGCAAAAGCAAAATTTTTAT
GATTTTAGAAACTTTTATTACAGTTTCACGTATGGACACTTACACTCAAT
ACCAGAATTTTTAGGGTCATCTATGATTTATTATGAATACGATTTAAGAA
AAGGAACCAAATCACATGTGTTTTTGGATCGAATCGATACGAAAAGGCTA
GAGAGGAGTCTTGACACTTCTTCCTATGGCAATGATAATATGGCAGCAAC
CAATAAAAATATTGCGATCTTAATTGATGACACCATAATTTTGAAAAATA
ATTTAATGTCAATGAGATTCATCAAACAGATTGATCGCTCGTTTACTGAG
AAGGTTAGAAAAGGACAAATAGCAAAGATATATGATTCCTTTTTGAACTC
TGTGAGGTTGAATTTTTTGAAGAATTATTCAGTTGAAGTATTGTGTGAAT
TTTTAGTAGCGTTGAACTTTTCAATCCGTAATATTTCGTCTTTATACGTA
GAAGAAGAAAGTGATTGCTCCCAAAGAATGAATTCTCCAGAGCTGCCAAG
GATCCACCTGAATAATCAAGCGCTTTCTGTCTTCAATTTACAAGGCTATT
ACTATTGCTTCATCCTAATTATCAAATTTTTATTGGATTTTGAAGCAACT
CCAAATTTTAAGTTACTGAGAATTTTTATTGAGTTGAGAAGCCTTGCGAA
TTCTATTTTACTTCCCACACTTTCAAGATTGTATCCGCAAGAGTTTTCTG
GATTTCCTGATGTTGTATTTACGCAACAATTTATAAATAAAGATAATGGT
ATGCTTGTCCCTGGTTTATCCGCAAATGAACACCATAATGGTGCAAGTGC
AGCTGTTAAGACTAAGTTAGCCAAAAAGATCAATGTTGAAGGGCTTGCAA
TGTTTATTAATGAAATCCTAGTTAACTCTTTTAACGATACCTCTTTTTTG
AATATGGAGGATCCTATTCGAAATGAATTTTCCTTTGATAATGGGGACAG
GGCAGTGACAGACTTGCCTCGTTCAGCACATTTCCTATCGGATACCGGCC
TAGAAGGTATTAACTTCAGCGGCTTAAATGATTCGCATCAAACTCTTTCT
ACTTTGAATCTTTTACGTTACGGGGAAAATCATTCATCAAAACATAAAAA
TGGTGGAAAGGGGCAAGGATTTGCCGAAAAGTACCAATTATCTCTGAAAT
ATGTTACTATTGCCAAGTTATTTTTCACCAATGTTAAAGAAAACTACATT
CATTGTCACATGTTAGATAAGATGGCAAGTGATTTCCACACTTTGGAAAA
TCATCTAAAGGGAAACAGTTGA

YDR216W, 1323 aa (SEQ ID NO 110)

MANVEKPNDCSGFPVVDLNSCFSNGFNNEKQEIEMETDDSPILLMSSSAS
RENSNTFSVIQRTPDGKIITTNNNMNSKINKQLDKLPENLRLNGRTPSGK
LRSFVCEVCTRAFARQEHLKRHYRSHTNEKPYPCGLCNRCFTRRDLLIRH
AQKIHSGNLGETISHTKKVSRTITKARKNSASSVKFQTPTYGTPDNGNFL
NRTTANTRRKASPEANVKRKYLKKLTRRASFSAQSASSYALPDQSSLEQH
PKDRVKFSTPELVPLDLKNPELDSSFDLNMNLDLNLNLDSNFNIALNRSD
SSGSTMNLDYKLPESANNYTYSSGSPTRAYVGANTNSKNASFNDADLLSS
SYWIKAYNDHLFSVSESDETSPMNSELNDTKLIVPDFKSTIHHLKDSRSS
SWTVAIDNNSNNNKVSDNQPDFVDFQELLDNDTLGNDLLETTAVLKEFEL
LHDDSVSATATSNEIDLSHLNLSNSPISPHKLIYKNKEGTNDDMLISFGL
DHPSNREDDLDKLCNMTRDVQAIFSQYLKGEESKRSLEDFLSTSNRKEKP
DSGNYTFYGLDLCTLSKISRALPASTVNNNQPSHSIESKLFNEPMRNMCI
KVLRYYEKFSHDSSESVMDSNPNLLSKELLMPAVSELNEYLDLFKNNFLP
HFPIIHPSLLDLDLDSLQRYTNEDGYDDAENAQLFDRLSQGTDKEYDYEH
YQILSISKIVCLPLFMATFGSLHKFGYKSQTIELYEMSRRILHSFLETKR
RCRSTTVNDSYQNIWLMQSLILSFMFALVADYLEKIDSSLMKRQLSALCS
TIRSNCLPTISANSEKSINNNNEPLTFGSPLQYIIFESKIRCTLMAYDFC
QFLKCFPHIKFDLSIKEKDVETIYIPDNESKWASESIICNGHVVQKQNFY
DFRNFYYSFTYGHLHSIPEFLGSSMIYYEYDLRKGTKSHVFLDRIDTKRL
ERSLDTSSYGNDNMAATNKNIAILIDDTIILKNNLMSMRFIKQIDRSFTE
KVRKGQIAKIYDSFLNSVRLNFLKNYSVEVLCEFLVALNFSIRNISSLYV
EEESDCSQRMNSPELPRIHLNNQALSVFNLQGYYYCFILIIKFLLDFEAT
PNFKLLRIFIELRSLANSILLPTLSRLYPQEFSGFPDVVFTQQFINKDNG
MLVPGLSANEHHNGASAAVKTKLAKKINVEGLAMFINEILVNSFNDTSFL
NMEDPIRNEFSFDNGDRAVTDLPRSAHFLSDTGLEGINFSGLNDSHQTVS
TLNLLRYGENHSSKHKNGGKGQGFAEKYQLSLKYVTIAKLFFTNVKENYI
HCHMLDKMASDFHTLENHLKGNS

YBR112C, 3401 bp, CDS: 501-3401 (SEQ ID NO 51)

GGGTGCCGTATCGGCTCTAATTATTTTATCTCTCTATTTTCTTTCTTTTTC
TCTGCGCTACTCCTTTCTCGATCGTTGCTACTCCCGTCGCTAGCCACTGG
TCTCCCGCGTACTGTACTCCATCTTTTTTTGGCGTTTTTCCCCTATCCAA
CTCGAACAAGGTTTGTTTAAATTTATTTATTTTCTTTTCTTCGGTCGG
TCGTTCTTTTCCCTTCCGATTATCAAAGCAAAAGCGCATTTTTTTCTTTG
TCTTTTTGTTTTTTGTTTCCTGTTCTCTGTTTTTTACAAACCACGTCAG
GAGTTCAATTGAGAGAACTAGAATCAACAAAGCCAAATACGACAACGTCA
CTAGTCTTTGAACCAGAGGCGTATTCCCGTTACCTCTTTTCCCATATTTC
TGTTTTTCTTTTTCACTGCTATAAGCCTTTAGACTAGTACTACAACTACA
ACAGCAACAACAACAAACAAAACACGACTGGAAAAAAAAAATTAGGAAAA
ATGAATCCGGGCGGTGAACAAACAATAATGGAACAACCCGCTCAACAGCA
ACAACAACAGCAACAACAACAGCAGCAACAGCAACAGCAGGCAGCAGTTC
CTCAGCAGCCACTCGACCCATTAACACAATCAACTGCGGAAACTTGGCTC
TCCATTGCTTCTTTGGCAGAAACCCTTGGTGATGGCGACAGGGCCGCAAT
GGCATATGACGCCACTTTACAGTTCAATCCCTCATCTGCAAAGGCTTTAA
CATCTTTGGCTCACTTGTACCGTTCCAGAGACATGTTCCAAAGAGCTGCA
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GGCTACTTTAGGTCATTGTTATCTGATGCTGGATGATCTGCAAAGAGCTT
ACAATGCCTATCAACAGGCTCTCTACCACCTCAGTAATCCCAACGTACCG
AAATTATGGCATGGAATCGGCATTCTTTATGACAGATATGGTTCGCTCGA
CTATGCCGAAGAAGCTTTTGCCAAAGTTTTGGAATTGGACCCTCATTTTG
AAAAGGCAAACGAAATTTACTTCAGACTAGGTATTATTTATAAACATCAG
GGTAAATGGTCTCAAGCTTTGGAATGCTTCAGATACATTCTCCCTCAACC
TCCTGCTCCCTTGCAGGAGTGGGACATATGGTTTCAGTTGGGTAGTGTTT
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TTGGCTCAAAATCAACATCATGCCAAAGTATTACAACAATTAGGTTGTCT

TTACGGTATGAGTAACGTACAATTTTATGACCCTCAAAAGGCATTGGATT
ATCTTCTAAAGTCGTTAGAAGCAGATCCCTCCGATGCCACTACATGGTAC
CATCTCGGTAGAGTGCATATGATTAGAACAGATTATACTGCCGCATATGA
TGCTTTCCAACAAGCTGTTAATAGAGATTCAAGAAACCCTATCTTTTGGT
GCTCAATCGGTCGTTTATATTACCAAATTTCTCAATACAGAGACGCCTTA
GACGCGTACACAAGAGCCATAAGATTAAATCCTTATATTAGTGAAGTTTG
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CCCTTGATGCGTATAAGCAAGCTGCAAGACTGGACGTAAATAATGTTCAC
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TATAAACAAATCGAACGGTGCGCCAACGAATGCCTCTCCTGCCCCACCTC
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AACACTAGAATTTCAGCCCAATCTGCCAATGCTACTGCTTCAATGGTACA
ACAACAGCATCCTGCTCAACAAACGCCTATTAACTCTTCTGCAACAATGT
ACAGTAATGGAGCTTCCCCTCAATTACAAGCTCAAGCTCAAGCTCAAGCT
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CACAAGCACATGCACAAGCGCAAGCACAAGCACAAGCACAGGCACAAGCA
CAAGCACAGGCGCAGGCACAACAACAACAACAACAACAGCAACAACAACA
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AGCAGCAGCAATTACAGCCCCTACCAAGACAACAGCTGCAGCAAAAGGGA
GTTTCTGTGCAAATGTTAAATCCTCAACAAGGGCAACCATATATCACACA
GCCAACAGTCATACAAGCTCACCAACTGCAACCATTTTCTACACAAGCTA
TGGAACATCCGCAAAGCTCTCAACTGCCACCTCAACAGCAACAACTACAA
TCTGTTCAACATCCACAACAACTTCAAGGCCAGCCTCAAGCCCAAGCTCC
CCAACCTTTAATCCAGCATAACGTGGAACAGAACGTTTTACCTCAAAAGA
GATACATGGAAGGTGCAATCCACACTTTAGTAGATGCCGCCGTATCCAGT
AGCACCCACACAGAGAATAACACAAAGTCTCCTCGTCAACCAACCCATGC
CATTCCAACGCAAGCTCCCGCAACAGGAATAACGAACGCTGAACCACAGG
TAAAGAAGCAAAAGTTGAACTCTCCAAATTCAAACATCAACAAATTAGTA
AATACTGCTACTTCCATTGAAGAAAATGCAAAATCTGAGGTGAGCAACCA
ATCGCCAGCAGTAGTGGAGTCTAATACCAATAATACTTCACAAGAAGAAA
AACCTGTAAAAGCAAACTCAATACCTTCAGTAATTGGCGCACAGGAACCT
CCACAGGAAGCTAGTCCTGCTGAAGAAGCTACCAAAGCAGCTTCTGTTTC
TCCTTCTACAAAACCGCTTAATACGGAACCAGAGTCATCTAGTGTCCAAC
CAACTGTATCATCAGAAAGTTCAACAACAAAAGCAAATGACCAAAGCACT
GCTGAGACCATAGAACTTTCTACTGCTACTGTTCCTGCAGAAGCAAGCCC
TGTAGAAGACGAAGTAAGACAGCATTCTAAAGAGGAAAACGGCACAACTG
AAGCATCTGCACCTTCTACTGAAGAGGCGGAGCCAGCAGCTTCCAGAGAT
GCTGAAAAACAACAAGATGAAACCGCTGCTACAACGATAACTGTAATCAA
ACCTACTTTGGAAACAATGGAAACAGTGAAAGAGGAGGCCAAAATGCGTG
AGGAAGAGCAAACATCTCAAGAAAAATCCCCACAGGAGAACACACTTCCA
AGAGAAAATGTAGTAAGGCAAGTGGAAGAAGATGAAAACTACGACGACTA
A

YBR112C, 966 aa (SEQ ID NO 52)
MNPGGEQTIMEQPAQQQQQQQQQQQQQQQAAVPQQPLDPLTQSTAETWL
SIASLAETLGDGDRAAMAYDATLQFNPSSAKALTSLAHLYRSRDMFQRAA
ELYERALLVNPELSDVWATLGHCYLMLDDLQRAYNAVQQALYHLSNPNVP
KLWHGIGILYDRYGSLDYAEEAFAKVLELDPHFEKANEIYFRLGIIYKHQ
GKWSQALECFRYILPQPPAPLQEWDIWFQLGSVLESMGEWQGAKEAYEHV
LAQNQHHAKVLQQLGCLYGMSNVQFYDPQKALDYLLKSLEADPSDATTWY
HLGRVHMIRTDYTAAYDAFQQAVNRDSRNPIFWCSIGVLYYQISQYRDAL
DAYTRAIRLNPYISEVWYDLGTLYETCNNQLSDALDAYKQAARLDVNNVH
IRERLEALTKQLENPGNINKSNGAPTNASPAPPPVILQPTLQPNDQGNPL
NTRISAQSANATASMVQQQHPAQQTPINSSATMYSNGASPQLQAQAQAQA
QAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAHAQAQAQAQAQAQA

QAQAQAQQQQQQQQQQQQQQQQQQQQQQQQQQQQLQPLPRQQLQQKG
VSVQMLNPQQGQPYITQPTVIQAHQLQPFSTQAMEHPQSSQLPPQQQQLQ
SVQHPQQLQGQPQAQAPQPLIQHNVEQNVLPQKRYMEGAIHTLVDAAVSS
STHTENNTKSPRQPTHAIPTQAPATGITNAEPQVKKQKLNSPNSNINKLV
NTATSIEENAKSEVSNQSPAVVESNTNNTSQEEKPVKANSIPSVIGAQEP
PQEASPAEEATKAASVSPSTKPLNTEPESSSVQPTVSSESSTTKANDQST
AETIELSTATVPAEASPVEDEVRQHSKEENGTTEASAPSTEEAEPAASRD
AEKQQDETAATTITVIKPTLETMETVKEEAKMREEEQTSQEKSPQENTLP
RENVVRQVEEDENYDD

YMR043W, 1361 bp, CDS: 501-1361 (SEQ ID NO 305)
AAGCTGTGCCAAACAAGGTCATCTCCAAATACTTACCAAAAAGCTAGGGC
GTACTGTACTGGAATCTCTGCTTTTTTCTTTACCTTACTTCAATTTGCCT
TGTCTGCTTTTTTACGTGTGTTTTGGCGTTTCTGCTTTTCTTTTTTTATTA
CTCGTTGTTGTAAATCATTTTCTAAGTATTATACATACTATATCATCGCA
TACCCAATCGGTTTCCTATTCTCACCACTTTTTTCTGGAAAAATACATAG
CCTAACAAGCAATTTTATTTTACGTTTGTTAATTCATTATACTGATAATA
TTTTTGAATTTTTTTTTTTTTTTGATACATTTTTTTAATCGCTGTTTTGT
CTGTTTTTTTCGATTCAGTTATAGGGAAAAAAACGGGAAAGGAAAGAGAA
AAAAAAATTAGTGCAGAGCAATAAGAAGCGAAAATCAAAAAAAAGTTTTG
GATCTGCAAGACTTGCTGTCACGCAACAATATTATAGCCACCCAGCAAAA
ATGTCAGACATCGAAGAAGGTACGCCTACTAATAATGGGCAACAGAAGGA
GAGAAGAAAGATAGAAATTAAGTTCATCGAGAATAAAACAAGGCGCCATG
TGACATTTTCCAAAAGGAAGCACGGTATCATGAAAAAGGCGTTTGAGCTT
TCTGTTCTAACGGGGACCCAGGTCCTGTTGCTAGTCGTTTCAGAAACAGG
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AGGAAGGTAGAAACCTGATCCAGGCCTGTCTTAACGCCCCTGATGATGAG
GAAGAAGACGAGGAGGAAGACGGTGATGATGATGATGATGATGACGATGA
TGGTAATGATATGCAACGCCAGCAACCACAACAACAGCAACCGCAACAAC
AGCAACAAGTATTGAATGCACACGCAAATAGCTTAGGCCATCTAAATCAA
GATCAGGTACCGGCAGGCGCGCTGAAACAAGAGGTGAAGTCACAATTGCT
AGGCGGTGCCAATCCTAATCAAAACTCAATGATTCAACAGCAGCAACATC
ACACGCAGAATTCACAACCACAACAGCAACAGCAACAACAACCACAGCAG
CAAATGTCACAGCAACAAATGTCACAGCATCCTCGACCACAGCAAGGAAT
ACCACATCCGCAACAATCGCAGCCACAGCAACAGCAACAACAACAACAAC
AACTGCAACAGCAGCAACAGCAGCAACAACAACACCCCTCACCGGCATT
CATCAGCCTCACCAACAGGCTTTGCCAACGCTGCCTCCCCCTATCTGAA
TGCTGAACAGAATGCTGCCTACCAACAATACTTTCAAGAACCGCAACAAG
GCCAATACTAA

YMR043W, 286 aa (SEQ ID NO 306)
MSDIEEGTPTNNGQQKERRKIEIKFIENKTRRHVTFSKRKHGIMKKAPEL
SVLTGTQVLLLVVSETGLVYTFSTPKFEPIVTQQEGRNLIQACLNAPDDE
EEDEEEDGDDDDDDDDGNDMQRQQPQQQQPQQQQVLNAHANSLGHLNQ
DQVPAGALKQEVKSQLLGGANPNQNSMIQQQQHHTQNSQPQQQQQQQPQQ
QMSQQQMSQHPRPQQGIPHPQQSQPQQQQQQQQQLQQQQQQQQQPLTGI
HQPHQQAFANAASPYLNAEQNAAYQQYFQEPQQGQY

YPL089C, 2531 bp, CDS: 501-2531 (SEQ ID NO 385)
TTCCACGTTCGCAAAAAATACTTCCACGGTGACGAAGTCTGTCTCAGTCG
TATATTAAATGCAGAAATCGTCTTATCATTATTGGGCTCTCTTAACGGCG
CAGCATCACCGGGTGATGAATGCCAAGCCGCAGAAAGAAAGAAAAAAATT
TACTTCAGATTTCTGATAAAAATAAAACGGAAGAGATGAAAGCTAATAAT
AGAAACAGCTCGATCTTCCTCTGAACAATAATAATTAAAGGACAGACAAA
AAGAAACGTAAGAAAGAAGCGAGCCTGTTCTAAAGTGTTCAACGACTGAT
TCAATTAGAACTGCCTACTCCTGATAGCCAACTCAACTTTTGACTCGTTA

AAGTAATTGAAAGCTGGCAAGCAGAATTATTCTTTTTTTTTTTCAAGGTT
TCTATCACGTTGTGAGGTTAATATCCCCCGGAGCAAACAGGCTGAAGCGT
GAAAAAAACTTAAATATTAAAGTGTCGCAAAACTATACTATAGATACAAC
ATGGGTAGACGGAAGATTGAAATCCAGAGAATTTCTGATGACAGAAATAG
GGCTGTCACGTTTATAAAACGTAAAGCTGGCCTTTTTAAGAAGGCCCATG
AACTATCCGTTCTTTGTCAAGTAGACATAGCCGTCATTATACTGGGTCC
AATAACACGTTCTATGAGTTTTCCTCTGTGGATACGAATGATTTAATCTA
TCACTACCAAAATGACAAAAACTTGCTTCACGAAGTGAAAGATCCTTCCG
ATTATGGAGACTTTCACAAAAGTGCATCCGTTAACATAAATCAAGACCTA
CTCAGGTCGTCTATGTCAAATAAGCCTTCGAAATCAAATGTTAAAGGAAT
GAACCAGTCAGAAAATGATGATGATGAGAACAATGATGAGGACGACGATG
ATCATGGCAATTTTGAGAGGAATTCAAATATGCATTCGAATAAAAAAGCC
TCTGATAAAAATATACCGAGTGCACACATGAAGTTGTTATCCCCGACCGC
ACTCATTTCAAAGATGGATGGTAGTGAGCAAAATAAACGTCATCCTGAGA
ACGCGCTGCCGCCTTTACAACATTTGAAAAGATTGAAACCGGATCCTTTG
CAAATAAGTAGAACTCCGCAACAGCAACAGCAGCAAAATATATCGAGACC
ATACCATAGTAGCATGTACAATCTTAACCAGCCTTCATCCAGTTCATCTT
CTCCTTCCACGATGGATTTTCCAAAATTACCAAGCTTTCAAAACTCTTCC
TTTAATGGTCGTCCTCCACCCATTTCCATTTCACCGAACAAGTTCAGTAA
GCCATTTACAAATGCATCCTCAAGGACCCCTAAACAGGAGCACAAAATTA
ACAATAGTGGCAGCAATAATAATGACAACAGCAACTACACTCAGTCACCA
TCTAATTCTTTGGAAGACTCTATTCAGCAGACTGTCAAAGCAAGAAGGAA
ATTGTCCGCCAGACCGGTACTTCGTGTGAGAATTCCGAACAACAATTTCA
GCAGTAATTCCGCTATTCCAAGTGAACCCTCCTCTGCCTCCTCCACATCG
GCCAACGGCAATAGTATGGGCTCTTCGCAGATAATGAAAGAAAACAAAAC
AAGTAGGTCTAGCAAAATTTCTCCACTATCCGCATCTGCCTCAGGCCCCT
TAACTCTCCAAAAAGGTAATAATGGCAGAATGGTAATAAAATTGCCAAAT
GCAAATGCGCCTAACGGTTCTAACAATGGTAATGGCAGTAACAATAACAA
TCACCCTTATCCTTTCGGAAGTGGGTCTTCACCTCTTTTTTCTGCAACAC
AGCCATACATTGCCACTCCCTTGCAACCATCGAATATTCCTGGCGGACCT
TTCCAACAAAATACATCTTTTTTAGCTCAAAGACAAACCCAGCAATACCA
ACAAATGTCTTTCAAAAAACAGAGCCAAACAGTACCATTAACTACAACAT
TAACCGGACGCCCCCTTCAACTTTTTCCGGCCCTGAAACCAGCAATGGC
CCTCCAACTGGTTCACTGCCATCGAAGTTCGTACATGATTTGATGAGTAA
TTCTCCAAATGTTTCTTCTATATCGATGTTTCCAGACTGGTCAATGGGAC
CCAACAGTGCCAAGCCGGGAAACACAAACAATCCTGGTACTTTCCCTCCC
GTACAGACGGCCGTAAACAACGGCAACTCCAGCAATATCAGCAGCACTAA
CAACACTAACAACAACAACAACAATAACAACAACAACAGCAGCAACAACA
ACAGCAACAACGGCAACGACAATAACAGTAACAATAGCAATAACAGTTAC
TATAGTAATAATGAAGATGCACCCGTAAATGGAGCTGCTATTTCAGAACA
TACTACCGATGGTGACTCGAACAATCAGTCCAACTCAAGTACATATGATG
CTGCTGCCACCGCATATAATGGAAATACCGGGCTGACTCCATACATAAAT
ACTGCTCAAACACCACTAGGCACTAAATTCTTTAATTTTTCGACTGATAT
TTCAGGAGAAAAAAATTCAAGCAAAATATAA

YPL089C, 676 aa (SEQ ID NO 386)
MGRRKIEIQRISDDRNRAVTFIKRKAGLFKKAHELSVLCQVDIAVIILGS
NNTFYEFSSVDTNDLIYHYQNDKNLLHEVKDPSDYGDFHKSASVNINQDL
LRSSMSNKPSKSNVKGMNQSENDDDENNDEDDDDHGNFERNSNMHSNKKA
SDKNIPSAHMKLLSPTALISKMDGSEQNKRHPENALPPLQHLKRLKPDPL
QISRTPQQQQQNISRPYHSSMYNLNQPSSSSSSPSTMDFPKLPSFQNSS
FNGRPPPISISPNKFSKPFTNASSRTPKQEHKINNSGSNNNDNSNYTQSP
SNSLEDSIQQTVKARRKLSARPVLRVRIPNNNFSSNSAIPSEPSSASSTS
ANGNSMGSSQIMKENKTSRSSKISPLSASASGPLTLQKGNNGRMVIKLPN
ANAPNGSNNGNGSNNNNHPYPFGSGSSPLFSATQPYIATPLQPSNIPGGP
FQQNTSFLAQRQTQQYQQMSFKKQSQTVPLTTTLTGRPPSTFSGPETSNG

PPTGSLPSKFVHDLMSNSPNVSSISMFPDWSMGPNSAKPGNTNNPGTFPP
VQTAVNNGNSSNISSTNNTNNNNNNNNNSSNNNSNNGNDNNSNNSNNSY
YSNNEDAPVNGAAISEHTTDGDSNNQSNSSTYDAAATAYNGNTGLTPYIN
TAQTPLGTKFFNFSTDISGEKNSSKI

YOR372C, 2165 bp, CDS: 501-2165 (SEQ ID NO 371)
AAAATCGTGGTTACTTTCATATTCCTTAAACACTTTACCACTGTTACTGT
GCGCGTTCGAGCGTAGCTTTCGTGGTGAATTTATTGTAAGATTCTCCAGC
TGGCTCGATAGTTCTGCCTCCTGCGTATCCATATCCATTTCGGTATGCTT
TTACTATTCAACCTAGTCGGCAATTTTTTCACCTGAATATTGTTGAACAC
TTCTGGCATCCTAGATACTCATCTGTATTTATTCATTATCTGTTGTGCAT
CGTTAATAGCATTCCAGTAAACAAGTTTAGGTCACTACCCGCATAAGCCT
TTTGGCGTTTGGCGTAACCCTCCTCGCGAAAAGAAACGGGACGCAAAAAA
AAAAAACAACAAAACAAGAACAAAACAAAACAAATAGGACAGAGCCTTAA
GGAGCTGCAAGGATCTTCTGAATATTTGGCATCGGCATTGTGGGTGGAAA
AAGTGTCCAAATTGGAATAAATTGGTCAGAATAGAGCATTGATTCCAACT
ATGGACAGAGATATAAGCTACCAGCAAAATTATACCTCAACTGGGGCAAC
TGCAACTTCCTCAAGACAGCCCTCTACGGACAATAATGCAGATACAAATT
TTTTGAAGGTAATGTCAGAATTCAAATATAATTTTAACAGTCCGTTACCT
ACAACGACTCAATTCCCCACGCCCTATTCTTCTAATCAGTATCAACAGAC
TCAAGATCATTTTGCCAATACAGACGCTCACAACAGTTCGAGCAACGAAT
CGTCGTTGGTAGAGAACAGTATATTACCGCATCATCAGCAGATACAACAG
CAACAACAACAACAACAACAACAACAACAACAGCAAGCTCTAGGTTC
ACTTGTACCTCCTGCTGTCACAAGGACAGATACAAGTGAGACTTTGGACG
ATATCAACGTTCAACCTTCTTCTGTTTTGCAGTTCGGCAACTCTTTACCC
AGCGAATTTTTGGTTGCATCCCCAGAGCAATTCAAAGAATTTTTGTTGGA
CTCTCCGTCCACCAATTTCAATTTCTTTCACAAAACTCCGGCAAAGACAC
CACTTCGATTTGTAACAGATTCTAACGGTGCTCAGCAAAGCACCACAGAG
AACCCAGGTCAACAACAGAATGTTTTTAGCAATGTCGATTTGAACAATCT
TTTGAAGAGTAATGGAAAAACACCCTCATCTTCATGCACCGGCGCATTTT
CACGCACTCCTCTGAGTAAGATTGACATGAATCTCATGTTCAATCAACCG
CTGCCGACATCTCCATCAAAAAGGTTCTCCTCCCTGTCGTTGACACCATA
TGGAAGAAAAATTCTGAATGACGTCGGTACACCTTATGCAAAAGCATTGA
TATCGTCTAACAGCGCGTTAGTGGATTTTCAGAAGGCAAGAAAGGATATT
ACCACTAATGCAACATCCATAGGGCTGGAAAATGCCAACAACATCTTACA
GAGAACGCCGCTAAGATCTAACAATAAAAAATTATTTATTAAAACCCCCC
AGGATACCATCAATAGCACTAGCACACTAACTAAGGACAACGAAAATAAA
CAGGACATATACGGCTCTTCACCGACTACCATCCAATTAAATTCATCAAT
AACTAAATCTATCTCCAAATTGGATAACTCTAGAATTCCCTTGTTAGCTT
CGAGATCAGATAACATTCTGGATTCCAATGTGGATGACCAATTGTTTGAT
TTGGGGTTGACAAGATTACCTTTATCACCAACACCAAATTGTAATTCTTT
GCATAGTACAACCCACAGGTACATCTGCCTTACAAATTCCTGAGCTACCCA
AGATGGGGTCTTTTAGAAGTGATACGGGAATCAATCCAATTTCAAGTTCA
AACACAGTTTCTTTTAAGAGCAAATCAGGCAATAATAATTCAAAGGGTCG
AATCAAAAAAAATGGGAAGAAACCTTCCAAATTTCAAATTATTGTGGCAA
ATATTGATCAATTTAACCAGGATACATCATCGTCATCTTTATCATCATCA
TTGAATGCAAGTTCGAGTGCAGGGAATTCAAATTCAAACGTAACAAAGAA
AAGAGCAAGTAAACTCAAAAGATCACAGTCTTTACTTTCTGATTCCGGAT
CGAAATCACAAGCAAGGAAAAGCTGTAATTCTAAATCTAATGGAAATTTA
TTCAATTCACAGTAA

YOR372C, 554 aa (SEQ ID NO 372)
MDRDISYQQNYTSTGATATSSRQPSTDNNADTNFLKVMSEFKYNFNSPLP
TTTQFPTPYSSNQYQQTQDHFANTDAHNSSSNESSLVENSILPHHQQIQQ
QQQQQQQQQQQQQALGSLVPPAVTRTDTSETLDDINVQPSSVLQFGNSLP
SEFLVASPEQFKEFLLDSPSTNFFHKTPAKTPLRFVTDSNGAQQSTTE

NPGQQQNVFSNVDLNNLLKSNGKTPSSSCTGAFSRTPLSKIDMNLMFNQP
LPTSPSKRFSSLSLTPYGRKILNDVGTPYAKALISSNSALVDFQKARKDI
TTNATSIGLENANNILQRTPLRSNNKKLFIKTPQDTINSTSTLTKDNENK
QDIYGSSPTTIQLNSSITKSISKLDNSRIPLLASRSDNILDSNVDDQLFD
LGLTRLPLSPTPNCNSLHSTTTGTSALQIPELPKMGSFRSDTGINPISSS
NTVSFKSKSGNNNSKGRIKKNGKKPSKFQIIVANIDQFNQDTSSSSLSSS
LNASSSAGNSNSNVTKKRASKLKRSQSLLSDSGSKSQARKSCNSKSNGNL
FNSQ

YDR224C, 896 bp, CDS: 501-896 (SEQ ID NO 111)
TTTCTTCAACAACGACGAGTTAACTATTGTGCTCTTTTTTTGAGCCACCA
AATACACTCCATTCCAATAGCTTCGCACAGTGAGGCGAAAATTTTGGAAC
AGCGCTAATGAATTATTTGTGAGCTCGGCGAGTTCAAATTTGAAGAAAAC
GCGGTTGGGTCGTTAACTATGGTTAGACGCTCAATGTCGCCCGAAAGGGA
AGGCTGTTCTCACTTTTTCGCGCGTTGCACCCTTTCTTCCGCGAAAAAAT
GAGAACGATGGATTTAAAATCAAGAGAATTGGCCTTAGTAGTGGCAAATA
CTACCTTGGTTGGTTATCTTGTAACGATTGGTAAGAAAGGGGCATCTCTG
TTTTCTTGATGTATATAAACAACATGATTTGATCATCTCAGATGGTCAGA
TTTATTAAAGACGTTTCTCTTTCCGCATTTTCGATTATTGTTATATTAAA
TTTATCCTATATAGACAAGTCAAACCACAAATAAACCATACACACATACA
ATGTCTGCTAAAGCCGAAAAGAAACCAGCCTCCAAAGCCCCAGCTGAAAA
GAAACCAGCCGCTAAAAAGACTTCCACTTCCACTGATGGTAAGAAGAGAA
GCAAGGCTAGAAAGGAAACATACTCTTCTTACATTTACAAAGTTTTGAAG
CAAACTCACCCTGACACTGGTATTTCCCAAAAGTCCATGTCTATCTTGAA
CTCTTTCGTTAACGATATCTTTGAAAGAATCGCTACTGAAGCTTCTAAAT
TGGCTGCGTATAACAAGAAGTCTACTATCTCTGCTAGAGAAATTCAAACC
GCTGTTAGATTGATCTTACCAGGTGAATTGGCTAAGCATGCTGTCTCTGA
AGGTACTAGAGCTGTTACCAAGTACTCTTCCTCTACTCAAGCATAA

YDR224C, 131 aa (SEQ ID NO 112)
MSAKAEKKPASKAPAEKKPAAKKTSTSTDGKKRSKARKETYSSYIYKVLK
QTHPDTGISQKSMSILNSFVNDIFERIATEASKLAAYNKKSTISAREIQT
AVRLILPGELAKHAVSEGTRAVTKYSSSTQA

YLR294C, 830 bp, CDS: 501-830 (SEQ ID NO 281)
ACCAACCAACTTCTTCCTTTGTCCTCAATATCAAAGAAAAAAAAAAAAAC
CCACTGCTCAGATGTTATAAGGAAGGGGTGTTAACTTATATACAGGTTCA
TCTACCAGTCACCAGTCCATACAAACTTGAACCGTCTGCGTACCAGTCCT
AATCAAAATGTTCCCTATCGCTTCCAGAAGAATACTGCTCAATGCTTCAG
TTCTGCCATTGAGACTGTGCAATAGAAATTTCACTACCACAAGAATATCC
TACAACGTCATACAAGATTTGTATTTGAGGGAACTAAAAGACACCAAACT
GGCTCCAAGTACCTTGCAAGATGCTGAAGGTAATGTTAAGCCTTGGAACC
CACCACAAAAACCAAATCTACCAGAATTGGAACTTCAAGGCCCAGAGGCT
TTAAAGGCTTACACCGAGCAAAATGTAGAAACTGCTCATGTTGCTAAAGA
GTCTGAAGAGGGTGAGTCAGAGCCAATTGAAGAGGATTGGCTAGTTTTGG
ATGATGCTGAGGAAACCAAAGAAAGTCATTGAACTTTTCATAGCATCCTC
CTTGTCGAAGAAAAAACAAACAGAACCACAAGCTGAACAAGATCATTATT
TTTGGCTTTCTTCCTCTCATCTTTTTATATTCGAATCCAGTACAATAAAG
AAAAAGCAAAATACACTACGCACTCTTTGTAATCAGCCACACAAAATGCA
GAATTTATTTTTTAAACAAAAAATACAATTGTACATAGACACGTCTTTAT
CTTTCCTATTACTACTATTCTTTTATTTCAATAACTATTACTTTCTAAGT
ATGACCTACGCTTCTTTGGTAAATAAATAA

YLR294C, 109aa (SEQ ID NO 282)
MMLRKPKKVIELFIASSLSKKKQTEPQAEQDHYFWLSSSHLFIFESSTIK
KKQNTLRTLCNQPHKMQNLFFKQKIQLYIDTSLSFLLLLFFYFNNYYFLS

MTYASLVNK

YMR256C, 683 bp, CDS: 501-683 (SEQ ID NO 319)
CTTTTCAGTTATTTACCTTCCTTTCTCTCACGTGTAAATATTTGTGTGTC
ATACACACCGCTAAAAACCTTTGCATCAACTTATACCCTACATTTCTATA
GACGCTATTTGGAAACAAGATGTAACCCTTTTTTTCTTTTAGTTTTGAGA
TTTGTACTCGTAAAGAGTACGTTTATTTATTTATTCAAATTTTATTCTTC
ATACCATGTAAATATAAGCGCATATAATCACTACGATCTTAGTACAGCTA
GAATTGCTGACGCTTACAATTGCTTTATTGTTTGATTATATGCACGTATA
CATATAGTGTCAGCAAAAAAAAAAAAAGGCAGTACTTGATTGGCTACGCC
GCGCATCGTCCGAGAAATCCGGCCTGGTAGGGGCAGGTTTGAAAAGGCGG
ATAGAAATAAAAGATGATATTATTTATTCATCCCATGAATAGTAGAACTC
GATATAAGATTCTAAACCAACAAGTACAGAAAGCAAAACAATAATAAATA
ATGGCTAATAAAGTTATTCAACTACAGAAAATCTTCCAATCTTCCACTAA
ACCTCTATGGTGGAGACATCCAAGGTCAGCTTTATACCTGTATCCATTTT
ATGCTATTTTTGCGGTAGCCGTCGTTACACCACTTCTATACATTCCAAAT
GCTATTAGAGGTATCAAAGCCAAGAAGGCATAG

YMR256C, 60 aa (SEQ ID NO 320)
MANKVIQLQKIFQSSTKPLWWRHPRSALYLYPFYAIFAVAVVTPLLYIPN
AIRGIKAKKA

YLR327C, 761 bp, CDS: 501-761 (SEQ ID NO 287)
TTCTCATACGTATGTTTTTTTAGATTATGCACCTTCTTTGCCACAGTAAA
TGTGGCGGGGAAGATGTTGAGCTAGCGCCGTGCACAGTGGAAGAGACGGA
GGCGATTGTGGGGTTTCATCGGATTGTGCGGGAAGAAGGCCTACACCGTG
TTGAGCCACCCCCCCCTCAGGAGTAAATTTACACAAACAGTGGTGGTGCC
TATGGTGGTATACGAGATAGTGATAGAAGCTGCTGGATTGGGGTAGAAAT
TTTGTAGGCGTTTATGGATATGGTATGGATATGGTATGGCTTGAGGTAGG
TAATCCAGACACCACTGGAAATATATATAAGGAGAGAGTTCTGGCAGGTA
GATTTGTACTCCTCTCTACCACTTTCTTCTACTCCTTTTATTATGTAATG
TTTATTATAAGCACAGCAAAAACGTTAAATAAATCTAATAAGATTTCATT
ATAACATAACATTAAAGCACACAAATTTCTAACACAAACACAATTCAAAC
ATGACCAGAACTAGCAAATGGACAGTCCACGAAGCAAAGTCTAACCCAAA
GTATTTCACCCATAACGGCAACTTTGGGGAGTCTCCCAACCACGTCAAGA
GAGGAGGCTATGGGAAAGGCAATTGGGGCAAGCCTGGCGATGAGATTAAT
GACTTAATCGATTCTGGCGAAATTAAGACAGTCTTCAACAAGACCAGAAG
GGGCTCTAACTCCCAAAACAATGAAAGAAGGCTTTCTGATTTGCAACAAT
ACCACATCTAA

YLR327C, 86 aa (SEQ ID NO 288)
MTRTSKWTVHEAKSNPKYFTHNGNFGESPNHVKRGGYGKGNWGKPGDEIN
DLIDSGEIKTVFNKTRRGSNSQNNERRLSDLQQYHI

YHR161C, 2414 bp, CDS: 501-2414 (SEQ ID NO 211)
GTCATGCGCGCAATAGGAAAGCGCACGAAACAAATGAGTAATTCGTAGGA
AACAATGCAGCCCCCAGGGTCAGCAACTGACGTGACTCAGCCTGGCTTTT
GTAGAAAAAGATGACGCCCTGGCAGAGAGGTGGGGGAATTGAGGGGTCCT
CGCTACCCACCTTAAGTATGGAAGAATATGATGAAGAATATGATGATAAC
TCTTGGAAGCGAGCGGCGGGTTCCATCACTTTTTACGGATTGGTAACACA
GGGGCCTCAGTTCGATACTTGGTATTCAGGCTTCCAGCGTTGGTGAGTTT
AGTTAGCGGTATGGTATGCACATGGTGTTGATGCTTGGTGGTAATCATTC
GTTAGGTGAATTGAGCAGTAGCGATATTAGATATATTTAGTATTTTATAG
CGTCTTTTTGGTGGGGGAGGAAGGACAAAACCTGTCTCGTAAATATAAAG
GGACTGTTCGATATCGCAGATACTAGAGTATAAATTTCGATTGAGGCGAG
ATGACAACATATTTCAAGTTGGTAAAAGGTGCTACCAAGATCAAGTCAGC

CCCGCCCAAACAGAAGTATCTGGATCCGATACTGTTGGGGACCAGCAATG
AAGAGGATTTCTATGAGATCGTGAAGGGTTTGGATTCCCGAATTAATGAC
ACGGCGTGGACTATTGTGTATAAATCGCTGTTGGTGGTTCATTTGATGAT
AAGGGAGGGTTCCAAAGATGTTGCATTGCGGTACTACTCTAGGAACCTGG
AGTTTTTTGACATTGAAAACATACGTGGCTCCAATGGCAGTGCGTCTGGA
GACATGAGGGCACTTGATAGATACGATAATTATCTGAAGGTGAGATGCAG
GGAGTTTGGTAAAATCAAAAAGGACTATGTGAGAGACGGCTATCGAACAC
TGAAGCTGAACAGTGGCAATTACGGAAGCTCCAGAAACAAGCAACACTCT
ATCAATATAGCACTAGATCATGTGGAGTCCCTAGAGGTACAAATACAAGC
CCTGATTAAAAACAAGTATACACAATATGATTTGAGTAACGAATTGATCA
TATTTGGTTCAAGCTGCTTATTCAAGACCTGCTAGCGCTATATAATGCT
CTCAACGAAGGTATCATAACTCTGCTGGAGTCTTTTTTCGAACTATCTCA
TCATAATGCAGAGAGAACTCTAGACCTGTACAAGACGTTTGTTGATTTGA
CCGAGCACGTTGTCAGGTACTTGAAGAGCGGGAAGACTGCGGGCTTGAAA
ATACCCGTCATCAAGCATATCACTACCAAACTGGTCAGATCGCTAGAAGA
ACATCTGATAGAGGATGATAAGACGCACAACACTTTTGTGCCCGTTGACA
GTTCTCAAGGAAGTGCTGGGGCCGTAGTAGCCAAATCTACTGCACAGGAA
AGGTTGGAGCAAATCCGGGAACAAAAAAGGATACTAGAGGCACAATTGAA
AAACGAACAAGTAGCGATTTCCCCTGCTCTAACTACTGTCACGGCGGCTC
AATCTTACAACCCGTTTGGAACAGACTCTTCTATGCATACTAACATTCCA
ATGGCTGTGGCTAATCAAACGCAACAGATCGCAAATAACCCATTTGTATC
TCAAACTCAGCCACAGGTGATGAATACACCAACCGCTCATACAGAGCCCG
CAAATTTAAACGTTCCTGAATATGCAGCGGTCCAACACACAGTGAACTTC
AACCCTGTACAAGATGCTGGCGTAAGTGCCCAACAAACGGGGTACTATTC
GATTAACAACCATTTAACACCCACATTTACAGGTGCAGGGTTTGGAGGAT
ACTCCGTTTCACAGGATACAACTGCCGCTTCTAATCAACAAGTCTCTCAT
TCACAAACTGGTTCTAACAACCCGTTCGCATTGCACAACGCCGCGACGAT
CGCAACAGGGAATCCTGCACACGAAAATGTCTTAAATAACCCATTTTCAC
GACCAAACTTTGATGAACAAAATACCAATATGCCGCTACAACAACAGATA
ATAAGTAACCCTTTTCAAAACCAAACGTACAATCAACAACAATTTCAACA
ACAAAAAATGCCTTTGAGCTCGATCAATAGCGTTATGACAACCCCTACTA
GCATGCAGGGATCGATGAATATTCCTCAGCGTTTTGATAAAATGGAATTT
CAGGCTCACTACACTCAGAATCATCTCCAACAACAGCAACAACAGCAACA
GCAACAACAGCAACAGCAACAACAGCAACCACAACAGGGTTATTATGTGC
CTGCAACTGCAGGAGCCAACCCTGTTACAAATATAACTGGGACAGTTCAA
CCTCAAAATTTCCCTTTCTATCCACAACAGCAACCACAACCGGAACAGTC
TCAAACACAGCAACCAGTTTTAGGAAACCAATATGCTAACAACCTCAATT
TAATTGATATGTAA

YHR161C, 637 aa (SEQ ID NO 212)
MTTYFKLVKGATKIKSAPPKQKYLDPILLGTSNEEDFYEIVKGLDSRIND
TAWTIVYKSLLVVHLMIREGSKDVALRYYSRNLEFFDIENIRGSNGSASG
DMRALDRYDNYLKVRCREPGKIKKDYVRDGYRTLKLNSGNYGSSRNKQHS
INIALDHVESLEVQIQALIKNKYTQYDLSNELIIFGFKLLIQDLLALYNA
LNEGIITLLESFFELSHHNAERTLDLYKTFVDLTEHVVRYLKSGKTAGLK
IPVIKHITTKLVRSLEEHLIEDDKTHNTFVPVDSSQGSAGAVVAKSTAQE
RLEQIREQKRILEAQLKNEQVAISPALTTVTAAQSYNPFGTDSSMHTNIP
MAVANQTQQIANNPFVSQTQPQVMNTPPTAHTEPANLNVPEYAAVQHTVNF
NPVQDAGVSAQQTGYYSINNHLTPTFTGAGFGGYSVSQDTTAASNQQVSH
SQTGSNNPFALHNAATIATGNPAHENVLNNPFSRPNFDEQNTNMPLQQQI
ISNPFQNQTYNQQQFQQQKMPLSSINSVMTTPTSMQGSMNIPQRFDKMEF
QAHYTQNHLQQQQQQQQQQQQQQQPQQGYYVPATAGANPVTNITGTVQ
PQNFPFYPQQQPQPEQSQTQQPVLGNQYANNLNLIDM

YLR206W, 2342 bp, CDS: 501-2342 (SEQ ID NO 277)
TACACCCTGACTTTCCCCATCATACGACGATGCTCTAGTAAACTTGCACC

CGCACCTGTTAGATAAACAAGTGCGCCCAAGATCACAATACCGAAGGGGC
GATATCACCACTCAGTATTCTACAGTCGAGCATAGCGTAGTCTGGCAGTA
TCCCGCACGATCCATTGTATTGTTTGTCCAAACCGCATTTTATGTGTAAC
GATTAATCGTATATACATGGCCTACAAGAAATTACCCTGCGGCGAAGGGT
GAAAAAAAAAGTAGTGGAAACTAAAGAAAGAAGAGTTTAGTTACGGACCC
TTTCAAGGATTGACACACTCCCAATATTTTGCTACATTATTGACCTTTGT
TGAAGGAGGCGTTCGTTTATTTAATTATTTTGTTCTGTTTTGCCTACAAC
TGCGAATACGCTCACATTCTAGTTTGACCTTCACAAATTCTTATCATCTT
CTTTTGTTTATTTTGACACACCCCTATTAAGTGTATTTGTTTTGTAAGTA
ATGTCTAAGCAGTTTGTTCGTTCTGCAAAGAACATGATGAAGGGCTACTC
ATCCACACAAGTGCTTGTGAGAGATGCCACGGCGAACGACTCGAGGACTC
CATCGATAGACACTCTCGACGATTTGGCACAGAGATCTTACGATTCGGTG
GACTTCTTCGAGATTATGGATATGTTAGACAAGAGGCTGAACGATAAGGG
CAAATACTGGAGACACGTTGCCAAATCGCTGACCGTTTTGGACTATCTTG
TTCGTTTCGGGAGTGAGAACTGTGTGCTATGGTGCAGAGAGAATTTTTAC
GTAATTAAGACATTAAGGGAATTCAGACACGAAAATGAGTCCGGATTTGA
CGAGGGACAAATTATCAGAGTAAAGGCTAAAGAACTCGTCTCTTTGTTGA
ATGATGAAGAAAGGCTACGCGAAGAGAGGTCTATGAATACAAGAAACAGA
AGGGCGAACAGAGCTGCTAGGCCAAGGCCAAGAAGACAAAGAACAAGGAG
CAACCCACACGATTCTTCTCCCTCTTACCAGGACGATTTGGAAAAGGCCC
TAGAGGAGAGCAGAATTACTGCTCAAGAAGATGAACAACGTAGAAGAGAA
CTGGCCCAGTACGACGATGAAGATCCTGACTTCCAAGCTGCCTTACAACT
AAGTAAAGAAGAAGAGGAGTTGAAGCAATTGCAGGAACTACAGAGATTAC
AGAAGCAACAACAGTCTCTGTCTCAATTTCAAGCTCCTTTACAACAACAA
CAACCACAACAACAACCAGCGTACTACGACATTTTCGGTAATCCAATCTC
CCAAGATGAATACTTACAGTATCAGTACCAACAGGACCAGGAACAAGCAA
TGGCTCAGCAAAGATGGCTGGACCAGCAGCAAGAACAACAGCAGCTTGCT
GAACAACAATATTTTCAGCAGCAACAACAAGCTGCGGCCGCCGCTTCTGC
CTTGCAACAGCAACAAACAGCCGCTAATATGCAACAACAACAACAACAGC
CCGCTGATTTTCAACAACCTTTGCCTACAGGTTCTAATAATCCGTTTTCC
ATGGATAATCTTGAAAGACAAAAGCAGGAGCAACAGCATGCTCAATTGCA
AAGACAACAAGAAGAAGCTAGACAACAACAAGAACAATTGAAGCTACAAC
AATTGCAAAGACAACAACAAGAGGAAGCTCAATTACACCAGAAGAGGCAA
GAAGAAGCCCAATTACAACAGCAGCAAGCCCAATTGCTACAACAGCAAGC
CCAGTTCCAGCAACAACAACCCTTGAAGCAAACAAGGACTGGGAACCAGT
CTATATCGGATAAATACAGCGACTTGAATACCTTGTTAGCAACTGGTACA
GGGATAGATACTTTTGGTAACACTGGAGAGGCACGTATTCCTGCACAACA
TACAAAGACAGGCACATTTATAAATTCTCAGGGTACAGGCTACAAACAGG
TTACTAATGAACCCAAGAACAACCCTTTCTTAAGCAACCAATACACTGGT
TTACCAAGCACAAATATCGTGCCCACGCAAACAGGGTACGGGTTTGGTAA
CCAACCTCAAAGTCCTCCTACTAATTCTCCTCAGCAAAATCCTACTGGTA
TAAGCTACTCTCAGCCACAACAGCAACAACAGCCACAGCAACAACCGCAA
TACATGCAAAATTTCCAACAACAGCAACCTCAATACGCCCAAAACTTCCA
ACAACAACCACAATACACTCAAAATTATCAACAACAACCACAATACATTC
AACCTCATCAACAACAACAGCAGCAGCAGCAGCAGCAACAGCAGCAACAG
GGATATACTCCTGACCAAGGTGTAAGCTTAATTGATCTTTGA

YLR206W, 613 aa (SEQ ID NO 278)
MSKQFVRSAKNMMKGYSSTQVLVRDATANDSRTPSIDTLDDLAQRSYDSV
DFFEIMDMLDKRLNDKGKYWRHVAKSLTVLDYLVRFGSENCVLWCRENFY
VIKTLREFRHENESGFDEGQIIRVKAKELVSLLNDEERLREERSMNTRNR
RANRAARPRPRRQRTRSNPHDSSPSYQDDLEKALEESRITAQEDEQRRRE
LAQYDDEDPDFQAALQLSKEEEELKQLQELQRLQKQQQSLSQFQAPLQQQ
QPQQQPAYYDIFGNPISQDEYLQYQYQQDQEQAMAQQRWLDQQEQQQLA
EQQYFQQQQQAAAAASALQQQQTAANMQQQQQQQPADFQQPLPTGSNNPFS
MDNLERQKQEQQHAQLQRQQEEARQQQEQLKLQQLQRQQQEEAQLHQKRQ

EEAQLQQQQAQLLQQQAQFQQQQPLKQTRTGNQSISDKYSDLNTLLATGT
GIDTFGNTGEARIPAQHTKTGTFINSQGTGYKQVTNEPKNNPFLSNQYTG
LPSTNIVPTQTGYGFGNQPQSPPTNSPQQNPTGISYSQPQQQQQPQQQPQ
YMQNFQQQQPQYAQNFQQQPQYTQNYQQQPQYIQPHQQQQQQQQQQQQQ
GYTPDQGVSLIDL

YDR342C, 2213 bp, CDS: 501-2213 (SEQ ID NO 119)
CACTTCTCAGAAATGCATGCAGTGGCAGCACGCTAATTCGAAAAAATTCT
CCAGAAAGGCAACGCAAAATTTTTTTTCCAGGGAATAAACTTTTTATGAC
CCACTACTTCTCGTAGGAACAATTTCGGGCCCCTGCGTGTTCTTCTGAGG
TTCATCTTTTACATTTGCTTCTGCTGGATAATTTTCAGAGGCAACAAGGA
AAAATTAGATGGCAAAAAGTCGTCTTTCAAGGAAAAATCCCCACCATCTT
TCGAGATCCCCTGTAACTTATTGGCAACTGAAAGAATGAAAAGCGAGGAAA
ATACAAAATATACTAGAACTGAAAAAAAAAAAAGTATAAATAGAGACGATA
TATGCCAATACTTCACAATGTTCGAATCTATTCTTCATTTGCAGCTATTG
TAAAATAATAAAACATCAAGAACAAACAAGCTCAACTTGTCTTTTCTAAG
AACAAAGAATAAACACAAAAACAAAAAGTTTTTTTAATTTTAATCAAAAA
ATGTCACAAGACGCTGCTATTGCAGAGCAAACTCCTGTGGAGCATCTCTC
TGCTGTTGACTCAGCCTCCCACTCGGTTTTATCTACACCATCAAACAAGG
CTGAAAGAGATGAAATAAAAGCTATGGTGAAGGTGAAGAGCACGAACCT
GTCGTTGAAATTCCAAAGAGACCAGCTTCTGCCTATGTCACTGTCTCTAT
TATGTGTATCATGATCGCCTTTGGTGGTTTCGTTTTCGGTTGGGATACTG
GTACCATTTCTGGTTTCATCAATCAAACCGATTTCATCAGAAGATTTGGT
ATGAAGCATAAAGATGGTACTAATTATTTGTCTAAGGTTAGAACTGGTTT
GATTGTCTCCATTTTCAACATTGGTTGTGCCATTGGTGGTATTATTCTTT
CCAAATTGGGTGATATGTACGGTCGTAAGGTGGGTTTGATTGTCGTTGTT
GTCATCTACATCATCGGTATTATTATTCAAATTGCATCTATCAACAAATG
GTACCAATATTTCATCGGTAGAATTATTTCCGGTTTGGGTGTTGGTGGTA
TTGCCGTTTTATCTCCTATGTTGATTTCTGAAGTATCCCCAAAGCATTTA
AGGGGTACTTTAGTCTCTTGCTACCAATTGATGATTACTGCCGGTATTTT
CTTGGGTTACTGTACCAACTTCGGTACTAAGAACTACTCCAACTCTGTGC
AATGGAGAGTTCCATTAGGTTTGTGTTTTGCCTGGGCTTTGTTTATGATT
GGTGGTATGACATTTGTTCCAGAGTCTCCACGTTATTTGGCTGAAGTCGG
TAAGATCGAAGAAGCCAAACGTTCTATTGCCGTTTCTAACAAGGTTGCTG
TTGATGATCCATCTGTTTTGGCTGAAGTCGAAGCTGTCTTGGCTGGTGTA
GAGGCAGAGAAATTAGCTGGTAATGCATCCTGGGGTGAATTGTTTAGTAG
CAAGACAAAGGTCCTTCAGCGTTTGATCATGGGTGCTATGATTCAATCTC
TACAACAATTGACAGGTGATAACTATTTCTTCTACTATGGTACTACTATT
TTCAAGGCTGTTGGTTTGAGTGACTCTTTCGAAACCTCTATTGTCTTGGG
TATTGTTAACTTTGCTTCCACCTTTGTTTGGTATTTACGTTGTTGAGAGAT
ATGGTCGTCGTACTTGTTTGCTATGGGGTGCTGCATCCATGACTGCTTGT
ATGGTTGTCTATGCTTCCGTGGGTGTCACCAGATTATGGCCAAATGGTCA
AGACCAACCATCTTCCAAGGGTGCTGGTAACTGTATGATTGTCTTTGCCT
GTTTCTATATTTTCTGTTTTGCTACTACATGGGCTCCAATTCCTTATGTC
GTTGTTTCTGAAACTTTCCCATTGAGAGTCAAGTCTAAGGCTATGTCTAT
TGCTACAGCTGCTAATTGGTTGTGGGGTTTCTTGATTGGTTTCTTCACTC
CATTTATTACTGGTGCTATTAACTTCTACTACGGTTACGTTTTCATGGGC
TGTTTGGTCTTCATGTTCTTCTATGTTTTGTTAGTTGTTCCAGAAACTAA
GGGTTTGACTTTGGAAGAAGTCAACACCATGTGGAAGAAGGTGTTCTAC
CATGGAAGTCTGCCTCATGGGTTCCACCATCCAGAAGAGGTGCCAACTAC
GACGCTGAAGAAATGACTCACGATGACAAGCCATTGTACAAGAGAATGTT
CAGCACCAAATAA

YDR342C, 570 aa (SEQ ID NO 120)
MSQDAAIAEQTPVEHLSAVDSASHSVLSTPSNKAERDEIKAYGEGEEHEP
VVEIPKRPASAYVTVSIMCIMIAFGGFVFGWDTGTISGFINQTDFIRRFG

MKHKDGTNYLSKVRTGLIVSIFNIGCAIGGIILSKLGDMYGRKVGLIVVV
VIYIIGIIIQIASINKWYQYFIGRIISGLGVGGIAVLSPMLISEVSPKHL
RGTLVSCYQLMITAGIFLGYCTNFGTKNYSNSVQWRVPLGLCFAWALFMI
GGMTFVPESPRYLAEVGKIEEAKRSIAVSNKVAVDDPSVLAEVEAVLAGV
EAEKLAGNASWGELFSSKTKVLQRLIMGAMIQSLQQLTGDNYFFYYGTTI
FKAVGLSDSFETSIVLGIVNFASTFVGIYVVERYGRRTCLLWGAASMTAC
MVVYASVGVTRLWPNGQDQPSSKGAGNCMIVFACFYIFCFATTWAPIPVV
VVSETFPLRVKSKAMSIATAANWLWGFLIGFFTPFITGAINFYYGYVFMG
CLVFMFFYVLLVVPETKGLTLEEVNTMWEEGVLPWKSASWVPPSRRGANY
DAEEMTHDDKPLYKRMFSTK

YDR343C, 2213 bp, CDS: 501-2213 (SEQ ID NO 121)
AAAAAAATGTTTTTTAGGCAACGGAGATTCGTTTATCCACGTTTACCCC
ACAAAAAGTGCAGGTACATTGTGGGGCCCCGGCATCGAAAACCAGTTTTT
TTCCTTTAAACGCTGGAAAAAAAGGAGAAATTATTGGAACTTTGCAGAGA
ATAGTCCGTAGGCAAATTGAAAATGTTCCTTAAAAAATTTCGTTTCTTAC
TCATTGAGATTATTCAGATGCCCTCCGTGCCTTCATTGAAAAAAATCCAA
GAGATGTCTCGGATCTGTATGCAGATTTTGGCTTGCAGACAATGGAGAGC
AAATGGGTATACAATATAGAAAGCACAGAAACATATAAAAAGAGCTCGAG
AAAAGACATATGGTTTGTAACTATCTTCTTTTTTCCAATTTTTCTGT
TTTAATAATAAAAAAACAAGAACAAACAAGCTCAACTTGTCTTTTCTAAG
AACAAAGAATAAACACAAAAACAAAAAGTTTTTTTAATTTTAATTCAAAAA
ATGTCACAAGACGCTGCTATTGCACACCAAACTCCTGTGGAGCATCTCTC
TGCTGTTGACTCAGCCTCCCACTCGGTTTTATCTACACCATCAAACAAGG
CTGAAAGAGATGAAATAAAAGCTTATGGTGAAGGTGAAGAGCACGAACCT
GTCGTTGAAATTCCAAAGAGACCAGCTTCTGCCTATGTCACTGTCTCTAT
TATGTGTATCATGATCGCCTTTGGTGGTTTCCTTTTCGGTTGGGATACTG
GTACCATTTCTGGTTTCATCAATCAAACCGATTTCATCAGAAGATTTGGT
ATGAAGCATAAAGATGGTACTAATTATTTGTCTAAGGTTAGAACTGGTTT
GATTGTCTCCATTTTCAACATTGGTTGTGCCATTGGTGGTATTATTCTTT
CCAAATTGGGTGATATGTACGGTCGTAAGGTGGGTTTGATTGTCGTTGTT
GTCATCTACATCATCGGTATTATTATTCAAATTGCATCTATCAACAAATG
GTACCAATATTTCATCGGTAGAATTATTTCCGGTTTGGGTGTTGGTGGTA
TTGCCGTTTTATCTCCTATGTTGATTTCTGAAGTATCCCCAAAGCATTTA
AGGGGTACTTTAGTCTCTTGCTACCAATTGATGATTACTGCCGGTATTTT
CTTGGGTTACTGTACCAACTTCGGTACTAAGAACTACTCCAACTCTGTGC
AATGGAGAGTTCCATTAGGTTTGTGTTTTGCCTGGGCTTTGTTTATGATT
GGTGGTATGACATTTGTTCCAGAGTCTCCACGTTATTTGGCTGAAGTCGG
TAAGATCGAAGAAGCCAAACGTTCTATTGCCGTTTCTAACAAGGTTGCTG
TTGATGATCCATCTGTTTTGGCTGAAGTCGAAGCTGTCTTGGCTGGTGTA
GAGGCAGAGAAATTAGCTGGTAATGCATCCTGGGGTGAATTGTTTAGTAG
CAAGACAAAGGTCCTTCAGCGTTTGATCATGGGTGCTATGATTCAATCTC
TACAACAATTGACAGGTGATAACTATTTCTTCTACTATGGTACTACTATT
TTCAAGGCTGTTGGTTTGAGTGACTCTTTCGAAACCTCTATTGTCTTGGG
TATTGTTAACTTTGCTTCCACCTTTGTTGGTATTTACGTTGTTGAGAGAT
ATGGTCGTCGTACTTGTTTGCTATGGGGTGCTGCATCCATGACTGCTTGT
ATGGTTGTCTATGCTTCCGTGGGTGTCACCAGATTATGGCCAAATGGTCA
AGACCAACCATCTTCCAAGGGTGCTGGTAACTGTATGATTGTCTTTGCCT
GTTTCTATATTTTCTGTTTTGCTACTACATGGCCTCCAATTCCTTATGTC
GTTGTTTCTGAAACTTTCCCATTGAGAGTCAAGTCTAAGGCTATGTCTAT
TGCTACAGCTGCTAATTGGTTGTGGGGTTTCTTGATTGGTTTCTTCACTC
CATTTATTACTGGTGCTATTAACTTCTACTACGGTTACGTTTTCATGGGC
TGTTTGGTCTTCATGTTCTTCTATGTTTTGTTAGTTGTTCCAGAAACTAA
GGGTTTGACTTTGGAAGAAGTCAACACCATGTGGGAAGAAGGTGTTCTAC
CATGGAAGTCTGCCTCATGGGTTCCACCATCTAGAAGAGGTGCCAACTAC
GACGCTGAAGAAATGGCTCACGATGATAAGCCATTGTACAAGAGAATGTT

CAGCACCAAATAA

YDR343C, 570 aa (SEQ ID NO 122)
MSQDAAIAEQTPVEHLSAVDSASHSVLSTPSNKAERDEIKAYGEGEEHEP
VVEIPKRPASAYVTVSIMCIMIAFGGFVFGWDTGTISGFINQTDFIRRFG
MKHKDGTNYLSKVRTGLIVSIFNIGCAIGGILSKLGDMYGRKVGLIVVV
VIYIIGIIIQIASINKWYQYFIGRIISGLGVGGIAVLSPMLISEVSPKHL
RGTLVSCYQLMITAGIFLGYCTNFGTKNYSNSVQWRVPLGLCFAWALFMI
GGMTFVPESPRYLAEVGKIEEAKRSIAVSNKVAVDDPSVLAEVEAVLAGV
EAEKLAGNASWGELFSSKTKVLQRLIMGAMIQSLQQLTGDNYFFYYGTTI
FKAVGLSDSFETSIVLGIVNFASTFVGIYVVERYGRRTCLLWGAASMTAC
MVVYASVGVTRLWPNGQDQPSSKGAGNCMIVFACFYIFCFATTWAPIPYV
VVSETFPLRVKSKAMSIATAANWLWGFLIGFFTPFITGAINFYYGYVFMG
CLVFMFFYVLLVVPETKGLTLEEVNTMWEEGVLPWKSASWVPPSRRGANY
DAEEMAHDDKPLYKRMFSTK

YGR192C, 1499 bp, CDS: 501-1499 (SEQ ID NO 183)
ACAGTTTATTCCTGGCATCCACTAAATATAATGGAGCCCGCTTTTTAAGC
TGGCATCCAGAAAAAAAAAGAATCCCAGCACCAAAATATTGTTTTCTTCA
CCAACCATCAGTTCATAGGTCCATTCTCTTAGCGCAACTACAGAGAACAG
GGGCACAAACAGGCAAAAAACGGGCACAACCTCAATGGAGTGATGCAACC
TGCCTGGAGTAAATGATGACACAAGGCAATTGACCCACGCATGTATCTAT
CTCATTTTCTTACACCTTCTATTACCTTCTGCTCTCTCTGATTTGGAAAA
AGCTGAAAAAAAAGGTTGAAACCAGTTCCCTGAAATTATTCCCCTACTTG
ACTAATAAGTATATAAAGACGGTAGGTATTGATTGTAATTCTGTAAATCT
ATTTCTTAAACTTCTTAAATTCTACTTTTATAGTTAGTCTTTTTTTTAGT
TTTAAAACACCAAGAACTTAGTTTCGAATAAACACACATAAACAAACAAA
ATGGTTAGAGTTGCTATTAACGGTTTCGGTAGAATCGGTAGATTGGTCAT
GAGAATTGCTTTGTCTAGACCAAACGTCGAAGTTGTTGCTTTGAACGACC
CATTCATCACCAACGACTACGCTGCTTACATGTTCAAGTACGACTCCACT
CACGGTAGATACGCTGGTGAAGTTTCCCACGATGACAAGCACATCATTGT
CGATGGTAAGAAGATTGCTACTTACCAAGAAAGAGACCCAGCTAACTTGC
CATGGGGTTCTTCCAACGTTGACATCGCCATTGACTCCACTGGTGTTTTC
AAGGAATTAGACACTGCTCAAAAGCACATTGACGCTGGTGCCAAGAAGGT
TGTTATCACTGCTCCATCTTCCACCGCCCCAATGTTCGTCATGGGTGTTA
ACGAAGAAAAATACACTTCTGACTTGAAGATTGTTTCCAACGCTTCTTGT
ACCACCAACTGTTTGGCTCCATTGGCCAAGGTTATCAACGATGCTTTCGG
TATTGAAGAAGGTTTGATGACCACTGTCCACTCTTTGACTGCTACTCAAA
AGACTGTTGACGGTCCATCCCACAAGGACTGGAGAGGTGGTAGAACCGCT
TCCGGTAACATCATCCCATCCTCCACCGGTGCTGCTAAGGCTGTCGGTAA
GGTCTTGCCAGAATTGCAAGGTAAGTTGACCGGTATGGCTTTCAGAGTCC
CAACCGTCGATGTCTCCGTTGTTGACTTGACTGTCAAGTTGAACAAGGAA
ACCACCTACGATGAAATCAAGAAGGTTGTTAAGGCTGCCGCTGAAGGTAA
GTTGAAGGGTGTTTTGGGTTACACCGAAGACGCTGTTGTCTCCTCTGACT
TCTTGGGTGACTCTCACTCTTCCATCTTCGATGCTTCCGCTGGTATCCAA
TTGTCTCCAAAGTTCGTCAAGTTGGTCTCCTGGTACGACAACGAATACGG
TTACTCTACCAGAGTTGTCGACTTGGTTGAACACGTTGCCAAGGCTTAA

YGR192C, 332 aa (SEQ ID NO 184)
MVRVAINGFGRIGRLVMRIALSRPNVEVVALNDPFITNDYAAYMFKYDST
HGRYAGEVSHDDKHIIVDGKKIATYQERDPANLPWGSSNVDIAIDSTGVF
KELDTAQKHIDAGAKKVVITAPSSTAPMFVMGVNEEKYTSDLKIVSNASC
TTNCLAPLAKVINDAFGIEEGLMTTVHSLTATQKTVDGPSHKDWRGGRTA
SGNIIPSSTGAAKAVGKVLPELQGKLTGMAFRVPTVDVSVVDLTVKLNKE
TTYDEIKKVVKAAAEGKLKGVLGYTEDAVVSSDFLGDSHSSIFDASAGIQ
LSPKFVKLVSWYDNEYGYSTRVVDLVEHVAKA

YOR374W, 2060 bp, CDS: 501-2060 (SEQ ID NO 373)

CGACCCTCTGGTTAGATGACACTCCTGCCCCAACTGCCACGAATCTGTAA
CCCCATAACTATACCCGTACGCAGTACTAAAAATGTATGTAATTAGTAAA
TGTATGTAACAATTTCACCGTTTTGTGTAACAATTCATTCATTCATTCTT
TTGATCCTTTAGTACCGTCCGCACATGATGTCATTTCCCCCTCATTTTTG
TTTGCTGGTATGATTCCCCGCCCGGGCGACGGTACGGCTGTTATCCAGCG
ATGCGGGACTTCCGTCCACAGGTATCTTTTTCTCCAACTCCAACAGAGAT
GGAAAATGAGGGGCGGGTGTAGGTAAGCAGAATGAGGAGAAATTTGTAAT
GAAAATGGAAGTTCGGCGGTTATATAAATGGGGGGGGTTTGTCGGTGACA
ATTGACTTCACTCTCCTTTCCTCAAAAATTCTTGGGTGTTAGGATTAGAA
GTATCTGGAAAACCAACCAAGAAAACTACAATAACAAAAATAAATAAAGC
ATGTTCAGTAGATCTACGCTCTGCTTAAAGACGTCTGCATCCTCCATTGG
GAGACTTCAATTGAGATATTTCTCACACCTTCCTATGACAGTGCCTATCA
AGCTGCCCAATGGGTTGGAATATGAGCAACCAACGGGGTTGTTCATCAAC
AACAAGTTTGTTCCTTCTAAACAGAACAAGACCTTCGAAGTCATTAACCC
TTCCACGGAAGAAGAAATATGTCATATTTATGAAGGTAGAGAGGACGATG
TGGAAGAGGCCGTGCAGGCCGCCGACCGTGCCTTCTCTAATGGGTCTTGG
AACGGTATCGACCCTATTGACAGGGGTAAGGCTTTGTACAGGTTAGCCGA
ATTAATTGAACAGGACAAGGATGTCATTGCTTCCATCGAGACTTTGGATA
ACGGTAAAGCTATCTCTTCCTCGAGAGGAGATGTTGATTTAGTCATCAAC
TATTTGAAATCTTCTGCTGGCTTTGCTGATAAAATTGATGGTAGAATGAT
TGATACTGGTAGAACCCATTTTTCTTACACTAAGAGACAGCCTTTGGGTG
TTTGTGGGCAGATTATTCCTTGGAATTTCCCACTGTTGATGTGGGCCTGG
AAGATTGCCCCTGCTTTGGTCACCGGTAACACCGTCGTGTTGAAGACTGC
CGAATCCACCCCATTGTCCGCTTTGTATGTGTCTAAATACATCCCACAGG
CGGGTATTCCACCTGGTGTGATCAACATTGTATCCGGGTTTGGTAAGATT
GTGGGTGAGGCCATTACAAACCATCCAAAAATCAAAAAGGTTGCCTTCAC
AGGGTCCACGGCTACGGGTAGACACATTTACCAGTCCGCAGCCGCAGGCT
TGAAAAAAGTGACTTTGGAGCTGGGTGGTAAATCACCAAACATTGTCTTC
GCGGACGCCGAGTTGAAAAAGCCGTGCAAAACATTATCCTTGGTATCTA
CTACAATTCTGGTGAGGTCTGTTGTGCGGGTTCAAGGGTGTATGTTGAAG
AATCTATTTACGACAAATTCATTGAAGAGTTCAAAGCCGCTTCTGAATCC
ATCAAGGTGGGCGACCCATTCGATGAATCTACTTTCCAAGGTGCACAAAC
CTCTCAAATGCAACTAAACAAAATCTTGAAATACGTTGACATTGGTAAGA
ATGAAGGTGCTACTTTGATTACCGGTGGTGAAAGATTAGGTAGCAAGGGT
TACTTCATTAAGCCAACTGTCTTTGGTGACGTTAAGGAAGACATGAGAAT
TGTCAAAGAGGAAATCTTTGGCCCTGTTGTCACTGTAACCAAATTCAAAT
CTGCCGACGAAGTCATTAACATGGCGAACGATTCTGAATACGGGTTGGCT
GCTGGTATTCACACCTCTAATATTAATACCGCCTTAAAAGTGGCTGATAG
AGTTAATGCGGGTACGGTCTGGATAAACACTTATAACGATTTCCACCACG
CAGTTCCTTTCGGTGGGTTCAATGCATCTGGTTTGGGCAGGGAAATGTCT
GTTGATGCTTTACAAAACTACTTGCAAGTTAAAGCGGTCCGTGCCAAATT
GGACGAGTAA

YOR374W, 519 aa (SEQ ID NO 374)

MFSRSTLCLKTSASSIGRLQLRYFSHLPMTVPIKLPNGLEYEQPTGLFIN
NKFVPSKQNKTFEVINPSTEEEICHIYEGREDDVEEAVQAADRAFSNGSW
NGIDPIDRGKALYRLAELIEQDKDVIASIETLDNGKAISSSRGDVDLVIN
YLKSSAGFADKIDGRMIDTGRTHFSYTKRQPLGVCGQIIPWNFPLLMWAW
KIAPALVTGNTVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKI
VGEAITNHPKIKKVAFTGSTATGRHIYQSAAAGLKKVTLELGGKSPNIVF
ADAELKKAVQNIILGIYYNSGEVCCAGSRVYVEESIYDKFIEEFKAASES
IKVGDPFDESTFQGAQTSQMQLNKILKYVDIGKNEGATLITGGERLGSKG
YFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMANDSEYGLA
AGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMS
VDALQNYLQVKAVRAKLDE

YER177W, 1304 bp, CDS: 501-1304 (SEQ ID NO 151)
AGATAGATAGATATAGATAGATAATGGACGTAGTTATAGAACAGAAAATC
GGTAGATCGAAAACACAGGGGAAAAAGGGGGGGGGGGGGGGAGACAGCG
CAGCCACGTGACGGGCTTCCTCTTTGGAAAGTGGAGCCGAAGTTTGCGGA
AGCTACTTTATTCCGGCCTGGAGTCAAAAGAGGAAGCTCGGTGGCAAATA
GCTTCCTCTTTGTGGCCGGGGCGCGGGGGGACGAGGCAAAAAGCAAAGAA
AAGCAAAAAAAATAAAAAAAAAAACAAAAAAACAGGGGTATGAGAAAAAG
ACACGCTTTTCCACGCGCAGCAAAAAGGAAAAAGGAAAAGGAAACTCTTT
ATTATTGGACCTTAAACCTGAAAACGAGACGAACCGTAACATAAAACCGT
GTAGTTTCTGCAAAAATAACTTAGTTTTTCCTACTTTTCAAAATTGAGAG
CGCAAGCAAGTGAGAAGAAAAAGCAAGTTAAAGATAAACTAAAGATAAAA
ATGTCAACCAGTCGTGAAGATTCTGTGTACCTAGCCAAGTTGGCTGAACA
GGCCGAACGTTATGAAGAAATGGTCGAAAACATGAAGACTGTTGCCTCCT
CTGGCCAAGAGTTGTCGGTCGAAGAGCGTAATTTGTTGTCTGTTGCTTAT
AAGAACGTTATTGGTGCTCGTCGTGCCTCTTGGAGAATTGTTTCTTCTAT
TGAGCAAAAGGAGGAGTCCAAGGAGAAGTCCGAACACCAGGTCGAGTTGA
TTTGTTCGTACCGTTCGAAGATTGAGACCGAACTAACTAAGATCTCCGAC
GATATTTTGTCCGTGCTAGACTCCCACTTAATTCCATCAGCCACCACTGG
CGAGTCCAAGGTTTTCTACTATAAGATGAAGGGTGACTACCACCGTTATT
TGGCTGAATTTTCTAGTGGCGATGCTAGAGAAAAGGCCACAAACGCCTCT
TTAGAAGCATACAAGACCGCTTCTGAAATTGCCACCACAGAGTTACCCCC
AACTCACCCAATCCGTCTAGGTTTGGCTCTTAACTTCTCTGTCTTCTATT
ATGAAATTCAAAACTCTCCAGACAAAGCCTGCCATTTGGCCAAGCAAGCT
TTTGACGACGCTATTGCTGAGTTGGACACTCTGTCTGAAGAATCATACAA
AGATAGCACACTTATCATGCAACTGCTAAGGGACAATTTAACCTTATGGA
CTTCAGACATGTCCGAGTCCGGTCAAGCTGAAGACCAACAACAACAACAA
CAACATCAGCAACAGCAGCCACCTGCTGCCGCCGAAGGTGAAGCACCAAA
GTAA

YER177W, 267 aa (SEQ ID NO 152)
MSTSREDSVYLAKLAEQAERYEEMVENMKTVASSGQELSVEERNLLSVAY
KNVIGARRASWRIVSSIEQKEESKEKSEHQVELICSYRSKIETELTKISD
DILSVLDSHLIPSATTGESKVFYYKMKGDYHRYLAEFSSGDAREKATNAS
LEAYKTASEIATTELPPTHPIRLGLALNFSVFYYEIQNSPDKACHLAKQA
FDDAIAELDTLSEESYKDSTLIMQLLRDNLTLWTSDMSESGQAEDQQQQQ
QHQQQQPPAAAEGEAPK

YOR267C, 2780 bp, CDS: 501-2780 (SEQ ID NO 363)
TAGTTCTATTTGGCTATATATTTCAGAGTGACAAATCTTTAAGAGAGACA
AACTGAGAATTAGCATATAGAATCATTCATACAACTGTTTACAAACAAGT
AAGCCCAAGACAGTTCCCAACCGCTTAAAGAAGTTTTTCCTAGAGGGAGC
AAAGTTCGTTTACATTTCACACACACAGTTTTTTTTCACTTTTTGGGCC
TCTTCCTTTTCCCGTTTTTTTCAAAAAGCTTAGAAATCTTCTTCACCTCC
TATTTTTCTAGAATCGTGAAGAATTTCCAGATTTAACAGTTTTCCACTTT
TTCAATAAGGAAATAGTAGGAATAATAAAAAAAGGATAGTAGTAACGATA
TACGTCGACTTTCCAGACTGGTCTCGAGCCGGAATTAAATACAATAGCAG
CGTTTGACTACCACATTGTAGCTCCGCTAGAATTGATCGAAAACAAAAAT
AATAACACTAATAATTATAATAATACGGTAGAACTATTTCTCGTATAAAG
ATGCCTAATCTATTGTCGAGAAACCCATTCCATGGTCATCATAATGACCA
TCATCATGACCGTGAAAATTCGTCTAATAACCCGCCACAGTTGATCAGAA
GTTCTAAATCTTTCTTAAACTTCATTGGTAGAAAACAAAGTAATGACTCA
CTAAGAAGCGAGAAATCTACAGATTCCATGAAATCTACCACAACCACTAC
AAATTATACTACAACAAACCTTAATAACAACACCCATAGCCATTCTAATG
CAACCAGTATCTCAACAAACAACTACAATAATAACTATGAAACAAACCAC
CACCATAATATTTCTCATGGGCTCCATGACTATACTTCTCCCGCCTCTCC

AAAACAAACCCACTCCATGGCAGAATTGAAAAGGTTTTCAGACCTTCTG
TAAATAAAAAACTATCTATGTCTCAACTTCGTTCCAAGAAACATAGCACC
CATTCCCCCCCACCTTCAAAATCAACTTCTACAGTTAATTTAAATAATCA
CTATCGTGCCCAGCATCCTCATGGCTTTACAGACCACTATGCTCATACCC
AGTCTGCTATACCGCCAAGTACCGATTCTATCCTATCTTTGTCCAATAAT
ATTAATATATATCACGATGATTGTATTCTGGCTCAAAAATACGGGAAATT
GGGTAAGTTATTGGGTTCCGGTGCCGGTGGGTCCGTTAAAGTTCTTGTGA
GACCAACTGATGGTGCTACTTTTGCCGTCAAAGAATTCAGACCAAGGAAA
CCGAATGAGAGTGTGAAAGAATATGCCAAGAAGTGCACCGCAGAATTTTG
TATTGGTTCGACTTTACATCACCCAAATGTTATCGAAACTGTTGACGTTT
TCTCTGATTCTAAACAAAATAAATACTATGAAGTTATGGAGTACTGTCCG
ATTGATTTTTTTGCTGTTGTTATGACAGGCAAGATGTCTCGTGGCGAGAT
CAACTGTTGCTTGAAGCAATTGACTGAAGGTGTTAAATATTTACATTCTA
TGGGATTGGCACATAGAGATTTGAAATTGGATAATTGTGTCATGACTTCC
CAGGGTATTTTGAAATTAATTGATTTTGGTAGTGCTGTTGTGTTCAGATA
TCCTTTTGAAGATGGCGTAACGATGGCTCATGGAATCGTGGGTAGTGACC
CTTACTTAGCGCCGGAAGTGATTACCTCCACCAAATCTTATGATCCTCAG
TGCGTCGATATATGGTCTATTGGGATCATATATTGTTGTATGGTGCTTAA
AAGGTTTCCATGGAAAGCCCCTAGAGATTCTGACGATAATTTTAGATTAT
ATTGTATGCCGGATGATATAGAACACGACTATGTTGAATCTGCCAGGCAT
CACGAAGAGTTACTGAAGGAAAGAAAAGAAAAGCGTCAAAGGTTTTTGAA
TCACAGTGACTGTTCCGCCATCAATCAGCAACAACCAGCTCATGAATCAA
ACTTGAAAACAGTTCAAAATCAAGTTCCAAATACTCCAGCATCTATACAG
GGTAAAAGCGATAACAAACCAGACATTGTGGAAGAAGAAACCGAAGAAAA
TAAAGAAGATGATAGCAATAATGATAAAGAAAGCACGCCAGATAATGACA
AGGAAAGTACCATCGATATTAAAATAAGCAAAAATGAGAATAAAAGCACG
GTAGTTTCAGCTAACCCAAAGAAAGTAGATGCCGATGCCGACGCTGATTG
CGATGCTAATGGTGACTCTAACGGCAGAGTGGATTGCAAGGCTAACAGTG
ACTGCAATGACAAAACGGATTGTAATGCTAACAATGACTGCAGCAATGAA
TCGGATTGTAACGCTAAAGTTGATACTAACGTCAACACTGCTGCCAACGC
TAACCCTGATATGGTTCCCCAAAACAATCCACCAACAACAACAACAACAAC
AACAACAACAACAACAACAACAACAACAACAACAACAACAACCCATCAT
CACCAGCATCAAAATCAAGACAAGGCCCATAGTATCGCTTCCGATAATAA
ATCGAGTCAACAGCACAGAGGACCTCACCATAAAAAAATTATTCATGGCC
CATACCGTCTATTACGTCTACTACCACATGCTTCAAGACCTATCATGTCC
CGTATACTGCAAGTAGATCCAAAGAAAAGAGCAACCTTAGATGATATTTT
TAATGATGAATGGTTTGCCGCCATTGCTGCCTGTACCATGGATTCAAAAA
ATAAAGTTATTAGAGCGCCTGGCCATCACCATACATTGGTTAGGGAGGAA
AATGCTCACTTAGAGACCTACAAGGTTTAA

YOR267C, 759 aa (SEQ ID NO 364)

MPNLLSRNPFHGHHNDHHHDRENSSNNPPQLIRSSKSFLNFIGRKQSNDS
LRSEKSTDSMKSTTTTNYTTTNLNNNTHSHSNATSISTNNYNNNYETNH
HHNISHGLHDYTSPASPKQTHSMAELKRFFRPSVNKKLSMSQLRSKKHST
HSPPPSKSTSTVNLNNHYRAQHPHGFTDHYAHTQSAIPPSTDSILSLSNN
INIYHDDCILAQKYGKLGKLLGSGAGGSVKVLVRPTDGATFAVKEFRPRK
PNESVKEYAKKCTAEFCIGSTLHHPNVIETVDVFSDSKQNKYYEVMEYCP
IDFFAVVMTGKMSRGEINCCLKQLTEGVKYLHSMGLAHRDLKLDNCVMTS
QGILKLIDFGSAVVFRYPFEDGVTMAHGIVGSDPYLAPEVITSTKSYDPQ
CVDIWSIGIIYCCMVLKRFPWKAPRDSDDNFRLYCMPDDIEHDYVESARH
HEELLKERKEKRQRFLNHSDCSAINQQQPAHESNLKTVQNQVPNTPASIQ
GKSDNKPDIVEEETEENKEDDSNNDKESTPDNDKESTIDIKISKNENKST
VVSANPKKVDADADADCDANGDSNGRVDCKANSDCNDKTDCNANNDCSNE
SDCNAKVDTNVNTAANANPDMVPQNNPQQQQQQQQQQQQQQQQQQQHHH
HQHQNQDKAHSIASDNKSSQQHRGPHHKKIIHGPYRLLRLLPHASRPIMS
RILQVDPKKRATLDDIFNDEWFAAIAACTMDSKNKVIRAPGHHHTLVREE

NAHLETYKV

YLR110C, 902 bp, CDS: 501-902 (SEQ ID NO 275)
TATTGGCGTCTGATTTCCGTTTTGGGAATCCTTTGCCGCGCGCCCCTCTC
AAAACTCCGCACAAGTCCCAGAAAGCGGGAAAGAAATAAAACGCCACCAA
AAAAAAAAAAATAAAAGCCAATCCTCGAAGCGTGGGTGGTAGGCCCTGGA
TTATCCCGTACAAGTATTTCTCAGGAGTAAAAAAACCGTTTGTTTTGGAA
TTCCCCATTTCGCGGCCACCTACGCCGCTATCTTTGCAACAACTATCTGC
GATAACTCAGCAAATTTTGCATATTCGTGTTGCAGTATTGCGATAATGGG
AGTCTTACTTCCAACATAACGGCAGAAAGAAATGTGAGAAAATTTTGCAT
CCTTTGCCTCCGTTCAAGTATATAAAGTCGGCATGCTTGATAATCTTTCT
TTCCATCCTACATTGTTCTAATTATTCTTATTCTCCTTTATTCTTTCCTA
ACATACCAAGAAATTAATCTTCTGTCATTCGCTTAAACACTATATCAATA
ATGCAATTTTCTACTGTCGCTTCTATCGCCGCTGTCGCCGCTGTCGCTTC
TGCCGCTGCTAACGTTACCACTGCTACTGTCAGCCAAGAATCTACCACTT
TGGTCACCATCACTTCTTGTGAAGACCACGTCTGTTCTGAAACTGTCTCC
CCAGCTTTGGTTTCCACCGCTACCGTCACCGTCGATGACGTTATCACTCA
ATACACCACCTGGTGCCCATTGACCACTGAAGCCCCAAAGAACGGTACTT
CTACTGCTGCTCCAGTTACCTCTACTGAAGCTCCAAAGAACACCACCTCT
GCTGCTCCAACTCACTCTGTCACCTCTTACACTGGTGCTGCTGCTAAGGC
TTTGCCAGCTGCTGGTGCTTTGTTGGCTGGTGCCGCTGCTTTGTTGTTGT
AA

YLR110C, 133 aa (SEQ ID NO 276)
MQFSTVASIAAVAAVASAAANVTTATVSQESTTLVTITSCEDHVCSETVS
PALVSTATVTVDDVITQYTTWCPLTTEAPKNGTSTAAPVTSTEAPKNTTS
AAPTHSVTSYTGAAAKALPAAGALLAGAAALLL

YLR109W, 1031 bp, CDS: 501-1031 (SEQ ID NO 273)
TGTCTATTAGTAATCAAGAAAAGAACCCTAAATCATCGGCGTCCCCTGTG
GGGCTCTCGGAAAAACCGGTCCTGACGTCACTGAAAAGATTTCGGCACAT
GGTCATGGGACCAGAGAAAAATTAATCCGACATGTGGAATATTTCCTTCC
GTTAAGGTAGTGAGCGCGGATTTTTTCTGATTTGTAATTATACGGGGAGC
TCTGGCCAAAAAGGTCAGTATTTGGTGATGAAGTTGAATATCATCTTTTG
ATTTTCTTCTGTATCATTCTTTTTCTTTTTCCACACCCCTTCCGGACGGT
ATTCACATATTGTTGAGAGGTTAAATGAAAAATAAAGGGGTGGAAAATTA
AGGACGAGATGTAAGGAAAAGCATAAACGAAACATTATATAAAGGAGCA
CAATTTCCTCTCCCTTGCCAATTGTGCATATACCGTTTCTTTATAACGAA
ATTTCAACAAACCAGAACAACACAAGTACTACCAATAACCACAACAAAAC
ATGTCTGACTTAGTTAACAAGAAATTCCCAGCTGGCGACTACAAATTCCA
ATACATTGCTATCAGCCAAAGTGATGCTGACAGTGAATCTTGTAAGATGC
CACAAACAGTTGAATGGTCCAAATTAATTTCTGAAAACAAGAAGGTTATC
ATTACCGGTGCTCCAGCTGCTTTCTCCCCAACCTGTACTGTCAGCCATAT
TCCAGGTTACATCAACTACTTGGATGAATTAGTTAAGGAAAAGGAAGTTG
ACCAAGTGATCGTTGTTACTGTTGACAACCCGTTCGCTAACCAAGCGTGG
GCTAAGAGTTTAGGTGTTAAGGACACCACACACATCAAGTTTGCCTCCGA
CCCAGGCTGTGCTTTCACCAAATCCATTGGTTTCGAATTAGCCGTCGGTG
ACGGTGTTTACTGGAGTGGTAGATGGGCCATGGTTGTTGAAAACGGTATC
GTTACTTACGCTGCCAAGGAAACCAACCCAGGTACCGATGTGACCGTTTC
CTCAGTCGAAAGTGTCTTGGCTCATTTGTAG

YLR109W, 176 aa (SEQ ID NO 274)
MSDLVNKKFPAGDYKFQYIAISQSDADSESCKMPQTVEWSKLISENKKVI
ITGAPAAFSPTCTVSHIPGYINYLDELVKEKEVDQVIVVTVDNPFANQAW
AKSLGVKDTTHIKFASDPGCAFTKSIGFELAVGDGVYWSGRWAMVVENGI
VTYAAKETNPGTDVTVSSVESVLAHL

YBL081W, 1607 bp, CDS: 501-1607 (SEQ ID NO 29)

TTGTTGCAACAATTTTGGGATGCTTCTGCGTCGTACGACCCTGTATTTAC
CTTCTCTAGCTCATCGCTTCCCAGGGTCCACGTTAATTTTTCAATTTTTT
CTTGCGTGTCGAAGATTCAGGTCTCGAGAAATTTGTCAAAAATTTTTCAC
TAGATATTAAGAACTATATACATCGAATAAGATGCCAGCACAGAAGAGAT
AGGCAATCAGTTTAGATACTACAGACACTATCCAATAGTGCAAAGCAAAA
GCAGCATAGAAAAAAGAGAATCCCGTTTCCAGCTTTTTCTCTTTTTCCCA
TTCGTTTTTCCTGATCTTTTTTTCTGCATCGTGGCACCTAGAACAAGAGG
TACCTTCCATCCTTCGCTTAATATTTGATACGACTTTTTGATTTCCATT
ATTATTATTTGTTACTATTATTATTTATCATTTGGGTTTCGGTTTTTTGT
AATAATTTTCTTTTTTTTTTTTGGCTCTATTTCACTAAGACATCGTATAT
ATGCCAGGCCAGATAATCAGCATTCCGTTTTTGTCGCAGAACGAGGACAT
GGATAAATACTTGTTGGAGTACCGCAGTTTGAAGCTCCTTCATCAGTCCA
GTAATTCCTTCCAGTCTCACAATGCGCCCTCCCACCAGTCGAACTACCAC
CCCCATTACAATCACATGAAATACAACAACACTGGTAGCTATTACTATTA
CAACAACAACAATAACAGCAGTGTAAACCCACATAACCAAGCTGGTCTAC
AATCCATTAACAGATCTATTCCATCGGCCCCGTACGGGGCTTACAACCAG
AACAGAGCTAATGACGTACCATATATGAATACCCAAAAGAAACACCACAG
ATTTAGCGCTAACAATAATTTGAACCAGCAAAAATACAAGCAATATCCCC
AGTATACGTCCAATCCAATGGTTACTGCACATCTGAAGCAAACGTACCCT
CAACTGTACTACAATAGCAACGTCAATGCTCACAACAACAACAACAACAG
CAACAACACAACAACAACAACAACAGCAACAACAACAACAATCATTT
ACAACCAGACGCAGTTCTCCACGAGGTACTTCAACTCGAACTCCTCTCCC
TCGTTGACTTCTTCCACTTCTAACTCATCCTCTCCATACAACCAAAGCAC
CTTCGAATACATTTTGCCGTCAACTTCGGCAGCTTCCACAAATTTATCGT
CGTCATCATCAAACAACTCTATGCACACCAACCCAACCACTGCAACATCG
ACATCCGCCGATTTAATCAATGATTTACCCGTGGGCCCCACGTCCAGTTC
GCTTATCTCGGATCTACATTCTCCACCAACTGTATCTTTCCTACCAGCAA
GCCAAACCCTGCTCATGTCCTCCACCACATCTAGCTCTATTGGCACCAAC
ATAAACCCACCGCCAACATTCACCATCCCCATCGCAAAGGGAGGATTTTTC
GACGGCACCAGTGAACATGTCTTCGTCCGCATCACTCTTGATGAATGATT
CTTCTTTAGGATGGGGGTCTAACCACATGAACGTATCTTCATCCTCTCAA
CCAGCATCATCAAGACCCTTTGGCATTTGGAATACTGACATGAGCGTTTG
GAGTTGA

YBL081W, 368 aa (SEQ ID NO 30)

MPGQIISIPFLSQNEDMDKYLLEYRSLKLLHQSSNSFQSHNAPSHQSNYH
PHYNHMKYNNTGSYYYYNNNNNSSVNPHNQAGLQSINRSIPSAPYGAYNQ
NRANDVPYMNTQKKHHRFSANNNLNQQKYKQYPQYTSNPMVTAHLKQTYP
QLYYNSNVNAHNNNNNSNNNNNNNNNSNNNNNLYNQTQFSTRYFNSNSSP
SLTSSTSNSSSPYNQSTFEYILPSTSAASTNLSSSSSNNSMHTNPTTATS
TSADLINDLPVGPTSSSLISDLHSPPTVSFLPASQTLLMSSTTSSSIGTN
INPPQHSPSPSQREDFSTAPVNMSSSASLLMNDSSLGWGSNHMNVSSSSQ
PASSRPFGIWNTDMSVWS

YDR366C, 899 bp, CDS: 501-899 (SEQ ID NO 125)

CTGTCGATATTGGGTTACTTTGTAGTGCATTATTTCCATCAATATTAGCA
GTGTCTTCCAAGGTGAACCATTGCGTGGTAAACCATAGAGTAAAAAAACA
AGTGGAAATGGTATCGATTGTATAAAGTACGCAGATTTGCGAAAATACCA
GCAAGTTTGGCTTATGAATCAAATACAGCCCTTGTGAGAATACGATTAAT
GTAAATACCGACCAAAGATATGCTATCCATTGCATAAAATCCAACGGATG
ACCCGTGAACAATGCTAAAATACCATAAGCACCACTGCATTTGTTTAGAA
TGGAAATACCTAAGACAATCTCAACTGCAAGGTATAGCGGCATAAACCCC
AAAAAAGACTATGAAAAAAAATATGTTTGAGAACAGGTTAGTAAAATTG
TGCTTTGCTTCGAATCCTTACAAGTTAACAAAAATTTATAGCGTTTGCCG
GAAACATACTTTTGGAAGGGTTAGAAGAGATGATCTCATAACTAAGGTTA

ATGGTTACAATTGGTAGTTCCTCCCTGGTATTATTTCTTTTCTTCGTAGT
TTTTGTACAGATCACTTATACAGCTTTACACAGATTTTCCCGCTTGTTGT
GCACTTTTTTTTCGAAGATTATTGAAGAGGGATGCGTTTGGTACAATAAA
AAACATAGGTTCCCAAACCTATATAAATATATATGTATATGTATATATAT
ACTACATATATGCTTTGAGAAATATGTGAATGTTGAGATAATTGTTGGGA
TTCCATTGTTGATAAAGGCTATAATATTAGGTATACAGAATATACTAGAA
GTTCTCCTCAAGGATTTAGGAATCCATAAAAGGGAATCTGCAATTCTACA
CAATTCTATAAATATTATTATCATCATTTTATATGTTTATATTCATTGA

YDR366C, 132 aa (SEQ ID NO 126)
MVTIGSSSLVLFLFFVVFVQITYTALHRFSRLLCTFFSKIIEEGCVWYNK
KHRFPNLYKYIYVVYVYILHICFEKYVNVEIIVGIPLLIKAIILGIQNILE
VLLKDLGIHKRESAILHNSINIIIIILYVYIH

YDR154C, 851 bp, CDS: 501-851 (SEQ ID NO 101)
TAGACGGGCTTCCACGCGCTTCCACTCATTTCTGTCTCTGGTAATGGCCG
TGGCCCTTCTCACTTTGGTTGGGCTTACGCTGACAAGTGTCTGTTCGATT
CCCTGTATAAATATAAACGTATTCTCTTGAGCCTTCTATCCTTTTGCCAC
TGTCGTCATCATTTGTTCCTCCTTTTTCGCTAGATAGGTTATATTAAGAT
TTGTCTTGAATTTAATATCTCAACTCAATCCAAACTCAACCGCTAATACT
ACCATGTCCCAAGTCTATTTTGATGTCGAAGCTGATGGCCAACCAATTGG
CCGTGTCGTTTTCAAGTTGTACAACGACATAGTCCCAAAGACTGCAGAAA
ACTTCAGAGCTCTATGTACCGGTGAAAAGGGATTCGGCTACGCTGGCTCT
CCATTCCACAGAGTTATTCCAGACTTCATGTTGCAAGGTGGTGACTTCAC
TGCTGGTAACGGTACCGGCGGTAAGTCTATCTACGGTGGCAAATTCCCAG
ATGAAAACTTCAAGAAGCACCACGACAGACCAGGTTTGTTGTCCATGGCC
AACGCCGGTCCAAACACCAACGGTTCTCAATTCTTCATCACCACCGTTCC
ATGCCCATGGTTGGACGGTAAGCATGTTGTCTTTGGTGAAGTTGTTGACG
GTTACGACATCGTTAAGAAGGTTGAGTCCTTGGGTTCTCCTTCCGGTGCC
ACCAAGGCTAGAATTGTTGTTGCCAAGTCCGGTGAATTATAACCGCTCTG
CCTGGAACAATACAGCAAAAATTGAAACGAACTATTCTCTCTTAAATTAT
ATGTATATGTATAAGGTATGTATGTATGACAATCAATTCTTATAACTA
A

YDR154C, 116 aa (SEQ ID NO 102)
MKTSRSTTTDQVCCPWPTPVQTPTVLNSSSPPFHAHGWTVSMLSLVKLLT
VTTSLRRLSPWVLLPVPPRLELLLPSPVNYNRSAWNNTAKIETNYSLLNY
MYMYKVCVCMTINSYN

YHR162W, 890 bp, CDS: 501-890 (SEQ ID NO 213)
CGCTCGCTTCCAAGAGTTATCATCATATTCTTCATCATATTCTTCCATAC
TTAAGGTGGGTAGCGAGGACCCCTCAATTCCCCACCTCTCTGCCAGGGC
GTCATCTTTTTCTACAAAAGCCAGGCTGAGTCACGTCAGTTGCTGACCCT
GGGGGCTGCATTGTTTCCTACGAATTACTCATTTGTTTCGTGCGCTTTCC
TATTGCGCGCATGACTAGGATGGAAAAAAAAAGAAGAAAAAGAAAAGCGT
TGAGTATATAATAAGAAAGAAGAAAAAGTCCGAGAGAAAAGAAGCACAAA
GGTTTTTCCTCGAGGAAAACAGTAAAGTTTGATACGCACATCGTTGACAT
CGCTGACTGCAATAGGAAACTGAAATAGACGGCAAACCATTAGTTCATTC
GAAAGAACGTATTGTCGAGAATTATCACTCACTATATCAGAAAATTGACA
CACGAATTATATAAACGAAGTTATACAGAAAAAGATTAAAGAAAAGAAAA
ATGTCTACATCATCCGTACGTTTTGCATTTAGGCGGTTCTGGCAAAGTGA
GACAGGCCCCAAGACGGTGCATTTCTGGGCTCCTACTTTGAAATGGGGTC
TGGTTTTCGCTGGATTCAGCGATATGAAGAGACCGGTGGAAAAAATTTCT
GGTGCTCAAAATTTGTCGCTGCTATCTACTGCGCTGATTTGGACTCGTTG
GTCCTTTGTCATCAAGCCAAGAAACATCTTGTTGGCTTCTGTCAACTCGT
TTCTTTGTCTGACCGCTGGCTATCAATTGGGTAGAATTGCCAACTACAGG

ATACGGAATGGCGACTCTATATCGCAATTGTGTAGCTATATTCTCAGCGG
CGCCGACGAAAGCAAAAAGGAAATTACTACGGGCAGATAA

YHR162W, 129 aa (SEQ ID NO 214)
MSTSSVRFAFRRFWQSETGPKTVHFWAPTLKWGLVFAGFSDMKRPVEKIS
GAQNLSLLSTALIWTRWSFVIKPRNILLASVNSFLCLTAGYQLGRIANYR
IRNGDSISQLCSYILSGADESKKEITTGR

YGR243W, 941 bp, CDS: 501-941 (SEQ ID NO 189)
CCTCCACCAAAGCAAAATGAAAACAAAGCCATACTGGGAAAAATCTGAAA
AAAAAAATGGTAGGAGTAAAAGAAAAGAAAAATAAAGGTTACCCTGCAG
TTTGGATAGTCGGGTAACATTTGGCCCTTTTCCTCCTTGATTGGATATTA
TTACCCCGATTACCCCTCATCTTGGGAGTGCCCCGCTTTTATTTCTCCCG
CCAATCGGCTATTAACGGCTTTACGTCATTCCGTGGGCGGGTCAAGCGAG
CCGCTCCCTGGTTTGGTCACGCAAAACCGAAAGGCTCAAACAAAACTAAG
GCCATCATATATATATGCGGCTGCGTGCGTGTATTCTCCCGGATAATA
TGGTGCGTTGCAATTGGAGTATTGGAGAAAATTTTCTTTTCCCTTTCATT
ACGGCGGAAATACTTCATATAAAAAAAAAGAATACAATCAGTCTTTAAGA
CTATACGCATAAGCATTCAAGACACATAGAAACACAAACCTATATTTTTA
ATGTCAGCATCAGCTTTTAATTTTGCCTTTAGAAGATTTTGGAATAGTGA
AACAGGCCCTAAAACAGTACACTTCTGGGCCCCAACTTTGAAGTGGGGGC
TGGTCTTCGCAGGGCTAAATGATATTAAGAGGCCTGTTGAGAAGGTATCA
GGAGCACAAAATTTATCTTTATTAGCGACGGCACTGATTTGGACGCGTTG
GTCGTTTGTCATCAAGCCCAAGAACTATCTGTTAGCTTCCGTCAATTTTT
TCCTGGGTTGCACTGCAGGCTACCATCTAACAAGAATTGCTAACTTTAGG
ATACGGAACGGTGATTCTTTTAAACAGGTTATTCACTACATAATAAAAGG
GGAGACTCCTGCAGCCGTCGCAGCAAAGCAAACTGCATCCACATCGATGA
ACAAAGGTGTGATCGGTACTAATCCGCCAATAACGCACTGA

YGR243W, 146 aa (SEQ ID NO 190)
MSASAFNFAFRRFWNSETGPKTVHFWAPTLKWGLVFAGLNDIKRPVEKVS
GAQNLSLLATALIWTRWSFVIKPKNYLLASVNFFLGCTAGYHLTRIANFR
IRNGDSFKQVIHYIIKGETPAAVAAKQTASTSMNKGVIGTNPPITH

YBR050C, 1517 bp, CDS: 501-1517 (SEQ ID NO 43)
AAGTACGATATGGTATAACTGTAACATTGAAGGACTGAAGGACTGAAGGA
CTGAAGGACTATAGTCAAGGGCCAATGGGGAAGGTCCCTTCCAGGCCATT
TGCCCGATAGTTTGTCCTTCTCTTGCTTTTCCGACGGCCCGATTGCATGT
GGCGGGGCAGCACTGGATAAAAAAACGTGGGGGGAGTGATTAAATTTATA
CGCTTATTGTGTCAACACGGAAACCTTATAGTTATCATTACTAACATCGC
AACAAGCTGCTTTTTTACTCGTTTTAGCCACACCATAACCCCTTTAATT
AACTAATAATGCATAAAATAGTTATTGCTTCTTGAGTTGCAGCTTCTTCC
TGGACGTACTGTTATATATGGCATGTCTTCGCATGTCCGTCAAATTTAGC
GTTGTCTCGAAACTTAGGCTGTCGTTCTTGCTGTCTGTCTTCTGATAAAA
TAATATATTGGAATAAGAAAAAAAAAATAGGAACAAGAAAGTGTGTGAGA
ATGACTTTGAGTAATTGCGACTCTTTGGATAACTTATTCCAGGACCCTCC
AGAGGAAGAAGAAAGTAGTAAATTCGTTGAGGCGGTCAGAACTTTGATGA
ATAGAAACGATATGGGATATCCTCCCGCCGCTGCAAATGGTACGTATTGC
TTAAAAAAAATCAAGTCTTTGAATGCCAAACAGTGGAAAATAAACAAGAA
AAGAATGTGCATGTTGCCAGCAGTAAAGAAGAAAAATTTCGACTTTCACG
AGCAAAGAAGTTTAATCTTGAATTTAAATTTATGGAAATTCATCAAGTTT
ATCAATTGTAGTAGTAAAAACAATTACAATAAAAATAATAAGCATGTGAG
AAGCTCGAACAACACTGTAAAAAATGAAAATGTTTTACCGTTACAAAAAC
ACAAGAAAGTGGACAATGATCAAAGATTGGAGAACCTTTTTTGGAGAAGC
TGGTTTAAGGCACGCAAAAGGAGAGATATAATGGGCAAGCCACGAGAGAG
GCATATCAAATTTAACGATAACGTTGAACAGTGTATTATAACTGATGAGC

ATTTCATACAAAGGCTTCCTTCTACACGGTTGAATTCGACTGATGAACAG
CGCCCTTGTTCAAAGTCTGAACTAGATCCCTGTATTGGCAACGCAGCAAG
TAAGCGAAGTTTCTATGATTATAACAGCGTTTACGTCGCGAGTGACGCAA
TTATTACGACTGCCGCTGCCACTGCCATTATCAGTAGTAATAGTGGAGAC
TATCAGCGTGGGCACGATGTTCGCGATGTTCCAAGAAATGTTTTGTTACA
GGCAGGAGAAACAGATTTCAGTAGTGTGCTTCGGGTTGACTCCGATCTCA
AGTTATCCAACATAAGTCATCATTCCCCCGTAAAACCTTCGTCAACTTCA
AGTCATTCGACCTTCATTTTCGAGTCGGAAACTGACACTGATACTGATAC
TGACGCTGAAACAGAAAATGACATTGACGCTTACATAGACACCAGTATAC
CCAACCTGCTCCTATAA

YBR050C, 338 aa (SEQ ID NO 44)
MTLSNCDSLDNLFQDPPEEEESSKFVEAVRTLMNRNDMGYPPAAANGTYC
LKKIKSLNAKQWKINKKRMCMLPAVKKKNFDFHEQRSLILNLNLWKFIKF
INCSSKNNYNKNNKHVRSSNNTVKNENVLPLQKHKKVDNDQRLENLFWRS
WFKARKRRDIMGKPRERHIKFNDNVEQCIITDEHFIQRLPSTRLNSTDEQ
RPCSKSELDPCIGNAASKRSFYDYNSVYVASDAIITTAAATAIISSNSGD
YQRGHDVRDVPRNVLLQAGETDFSSVLRVDSDLKLSNISHHSPVKPSSTS
SHSTFIFESETDTDTDTDAETENDIDAYIDTSIPNLLL

YEL071W, 1991 bp, CDS: 501-1991 (SEQ ID NO 143)
TAGCTTGACCTGGTCAGATTAATCAGCTTCCAACGTTACTTCCCTTTCGC
AAGAATCTACCCAAAATGTCTCGAGCATCTTGATAATTACAGTATCGTTC
GTCCCGACTTGGCATTTGTTTAAATTTCTAAGATGCTTCCTATAGGAACA
TAATTGTCAAGAAAGCACAACAAATTGTCTGCAATGTCAACAGGAGTGGC
GCATTTTATGTTTTTTCATTTTTTTTTTTTTGTGCGTGATCATTAAGCGG
GATATTGTCCACAGTCATCTAAAAGAATGACCATTTCGACGACTTAGTTC
GGAAAATATTTCCAGCGGATGACACCACTTGCCACAGTTGGTGACCGCCA
AATCTAAGTCACGCGCGGAAACTGAAAGGTTGTGAGTATATAAGTGATCA
CTCGCTTATATAACTGACGAGGCAGAACAGGGTGCCAAAATGCTCCTCAA
TATTTTATTCATTTGAGATTCAAGGCTTAAAGACAGCATATATAAGAATT
ATGACGGCCGCACATCCTGTTGCTCAGTTAACTGCCGAGGCATACCCTAA
AGTCAAGAGAAACCCAAATTTCAAAGTTCTCGACTCGGAAGATTTGGCGT
ACTTTCGTTCGATTTTGTCAAATGATGAAATCTTAAACTCTCAAGCTCCA
GAAGAGCTTGCTTCGTTTAACCAGGACTGGATGAAAAAATATAGAGGCCA
GTCCAATTTAATTCTCTTGCCAAACTCCACTGATAAAGTGTCCAAGATTA
TGAAATACTGTAACGATAAAAAGTTGGCAGTAGTACCACAAGGTGGTAAC
ACCGACTTGGTCGGAGCCTCTGTTCCGGTATTTGATGAGATTGTTCTTTC
TCTAAGAAATATGAACAAAGTCAGAGATTTTGATCCAGTTAGCGGGACTT
TCAAGTGTGACGCGGGTGTCGTTATGCGTGATGCGCATCAATTTTTACAC
GACCATGACCATATCTTCCCATTGGATCTGCCTTCTAGAAACAACTGTCA
AGTGGGCGGTGTAGTTTCAACAAATGCAGGTGGTTTGAACTTTTTAAGAT
ATGGGTCTCTACACGGTAATGTTTTGGGTTTGGAAGTGGTGCTACCCAAC
GGTGAGATTATCAGCAATATCAATGCCCTAAGGAAGGACAATACTGGTTA
TGACTTGAAACAATTATTCATCGGTGCAGAGGGTACTATCGGTGTCGTTA
CTGGTGTATCCATAGTTGCAGCAGCAAAGCCAAAAGCCTTGAATGCCGTA
TTTTTTGGTATTGAGAATTTCGATACCGTTCAGAAATTATTTGTCAAGGC
TAAAAGTGAATTATCTGAGATTTTATCTGCTTTTGAATTCATGGACCGTG
GCTCCATTGAATGTACGATAGAATACTTGAAGGACTTGCCTTTCCCTCTG
GAGAACCAACACAACTTTTATGTTCTTATTGAAACGTCAGGGTCCAATAA
GAGACACGACGATGAGAAGCTGACTGCTTTCCTCAAAGATACCACAGATT
CTAAATTAATTTCGGAGGGTATGATGGCTAAGGACAAAGCCGATTTTGAT
AGACTTTGGACCTGGAGAAAATCTGTTCCAACAGCTTGTAATTCTTACGG
TGGTATGTACAAGTATGACATGTCACTTCAATTGAAAGATTTATATTCCG
TATCTGCGGCTGTGACGGAGAGATTAAACGCAGCCGGTTTGATTGGTGAT
GCACCAAAACCAGTTGTTAAATCATGTGGTTATGGTCATGTCGGTGACGG

AAACATCCATTTAAATATCGCGGTAAGAGAATTTACAAAACAGATTGAGG
ACTTACTAGAACCATTTGTTTATGAATATATTGCATCAAAGAAAGGTTCC
ATCAGTGCTGAGCATGGGATCGGTTTCCATAAGAAAGGTAAGTTACACTA
CACCAGAAGTGATATTGAAATTAGATTTATGAAGGATATCAAAAATCACT
ACGATCCAAATGGAATCTTAAACCCATACAAGTACATTTGA

YEL071W, 496 aa (SEQ ID NO 144)
MTAAHPVAQLTAEAYPKVKRNPNFKVLDSEDLAYFRSILSNDEILNSQAP
EELASFNQDWMKKYRGQSNLILLPNSTDKVSKIMKYCNDKKLAVVPQGGN
TDLVGASVPVFDEIVLSLRNMNKVRDFDPVSGTFKCDAGVVMRDAHQFLH
DHDHIFPLDLPSRNNCQVGGVVSTNAGGLNFLRYGSLHGNVLGLEVVLPN
GEIISNINALRKDNTGYDLKQLFIGAEGTIGVVTGVSIVAAAKPKALNAV
FFGIENFDTVQKLFVKAKSELSEILSAFEFMDRGSIECTIEYLKDLPFPL
ENQHNFYVLIETSGSNKRHDDEKLTAFLKDTTDSKLISEGMMAKDKADFD
RLWTWRKSVPTACNSYGGMYKYDMSLQLKDLYSVSAAVTERLNAAGLIGD
APKPVVKSCGYGHVGDGNIHLNIAVREFTKQIEDLLEPFVYEYIASKKGS
ISAEHGIGFHKKGKLHYTRSDIEIRFMKDIKNHYDPNGILNPYKYI

YDR133C, 836 bp, CDS: 501-836 (SEQ ID NO 95)
GTGCAGAGGGTGAATCAACGGCCCCTTCACAGAAACCGCGCAGGAATTTT
TCTGGTGTTTGTTATTTTTTTTTCCTTGTACTTATCTCACTTTTCTTTTT
CTAACTATTTTTTTTGCAATTTTTTTGTGTACACTTTCCACAACATATAG
GATGGTTTAGTCATCTCTCGAAGTATATAAACCGTTGCTGGATCGTGGTT
GTTCTTCATCGACTTCTCTCTGCTAGACTCTCTTTTTTAAAATTTTTTCA
TAGAATAAAAAACCAAGGATAACAAACATCTTCTTTCGTTCGCTTCAAAA
TAACTACAAATTAAAAATGCAATTCTCTACCGTCGCTTCTATCGCTGCTA
TTGCCGCTGTTGCCTCCGCCGCTTCTAACATTACCACTGCTACTGTCACA
GAAGAATCTACCACTTTGGTCACTATCACTTCTTGTGAGGACCACGTTTG
TTCTGAAACAGTTTCCCCAGCTTTGGTTTCCACTGCTACCGTCACCGTAA
ATGACGTTATCACTTAATACACCACCTGGTGTCCATTGCCAACCACTGAA
GCACCAAAGAATACCACTTCTCCAGCTCCAACTGAAAAGCCAACCGAAAA
GCCAACTGAAAAGCCAACCCAACAAGGTTCTAGCACTCAAACTGTTACCT
CCTACACTGGTGCCGCTGTTAAGGCTTTGCCAGCTGCCGGTGCTTTGTTG
GCTGGTGCTGCCGCTTTATTGTTGTAATTTACTCAACCTTTTCTTTAATA
TATTTTTAGAAAAATGGTTAAGTACTTTTCCGTCAATACAGCTTCCACAA
AATCGTTTTATTTCAATTAATAAGATATTCTGGTAA

YDR133C, 111 aa (SEQ ID NO 96)
MTLSLNTPPGVHCQPLKHQRIPLLQLQLKSQPKSQLKSQPNKVLALKLLP
PTLVPLLRLCQLPVLCWLVLPLYCCNLLNLFFNIFLEKWLSTFPSIQLPQ
NRFISINKIFW

YHL021C, 1898 bp, CDS: 501-1898 (SEQ ID NO 193)
GGTAAAAGAAATGATCAGGGAGCGTTTCTTGCAACAGCAGCAACAGTACA
GGCAGCAACAGCAGAAGGATGGCAATTACGTAAAGCCCTCTCAGGACAAC
GTGGATAGCAAGGACTAACCGAGACAGATTGAGGTCTTTCATGCATTACC
ACCAGTAATAATTATTATACGGAATAATATAGTTTATATAATATCCATAAT
CATAATCATAATCATAATCATAATCATAATCGTGATATTGTACCAGCCCC
GCTTCTCCCCTTTTGAACTACCATTATTATCGGACCCTCTTTACCTTTGA
ATGGCTCAGTAAGGACCTTTGCGCAGCCGTAAGGGGGTCGGGAATACATT
TCCGGGGTTGATCCTCGAGGAAAAGTGCTATCTATATAAGGAGAAGCCCT
TCTAGATCCAAATATCAGGGGTAACTCTTCACAACTGGCCAGGAACATAT
TCCAAGTTAAAAAGAAAAAATAATTATTAGAAACCAATTACCAACACAAG
ATGCTAAGATCAAATTTATGCAGAGGATCTCGAATCCTTGCAAGACTGAC
CACTACACCAAGGACATACACATCTGCGGCGACAGCTGCGGCTGCGAATC
GGGGACATATCATCAAAACATACTTCAATAGAGATTCTACGACAATTACG

TTCTCCATGGAGGAGTCCAGCAAGCCGGTTTCCGTTTGCTTTAACAACGT
TTTTCTTAGAGATGCCTCCCATAGTGCCAAGCTGGTGACCACGGGAGAAC
TGTATCATAACGAGAAATTGACCGCTCCTCAGGACATTCAAATTTCTGAG
GACGGAAAATCTCTAGTGGTGAAATGGAAAGATGGCGGTCATCACCAGTT
CCCTTTACAATTCTTTATCGACTATAAAGGTTCCAGTTTTGTTTCGCCAG
CAACAAGAAAACAAGAATCCAGATATAGACCCCAGTTATGGAATAAGCGC
ATCCTGAAAGATAACGTCAAGGACTTACTTTCTGTGAGCTACAACGAGTT
TATTGATCCTAAGGATGACTCCAAGCTTTTCCAAACGCTGGTCAACCTAC
AAAAGTTTGGTATCGCTTTCATTTCCGGTACTCCTTCATCCTCCTCTGAA
GGCCTTACCATACAAAAGATCTGTGAAAGGATCGGACCCATAAGATCGAC
TGTACATGGTGAAGGTACATTTGACGTGAATGCATCCCAAGCGACAAGTG
TTAATGCCCATTATGCCAATAAAGACTTGCCGCTACATACGGATTTACCA
TTTTTAGAAAATGTGCCAGGTTTCCAGATTCTACAATCTCTACCTGCTAC
AGAAGGGGAAGATCCCAATACTAGACCCATGAATTACTTCGTGGACGCAT
TTTATGCTACCCGTAATGTTAGAGAATCGGATTTTGAGGCTTATGAGGCT
TTACAAATTGTTCCTGTAAATTATATATATGAAAACGGCGATAAGAGGTA
CTACCAATCCAAACCTTTAATCGAACATCACGACATTAACGAGGACAATA
CTCTTCTGGGTAATTATGAGGCCTTGATTAAATGCATTAACTACTCTCCA
CCATACCAAGCACCTTTCACTTTCGGAATTTATGATAAGCCCTCAGATCT
AAATAATAATCTGGACTTGAATTTAATTACCACCCCAGCAAAACTAACAG
AGAGATTTTTGTTTAAGTCTTTCATTAGGGGGTTGAACTTGTTCGAGAGT
CATATCAATGACTTCAACAATCAATTTAGATTGCAGTTGCCCGAAAACTG
TTGTGTTATCTTTAACAACAGGAGAATTTTGCATGCTAACTCTTTAACAA
GCTCAAACCAGCAATGGTTAAAGGGTTGCTATTTCGATTCTGATACTTTC
AAGAGTAAATTAAAGTTCTTGGAAGAGAAGTTTCCTCATGACAAATAA

YHL021C, 465 aa (SEQ ID NO 194)
MLRSNLCRGSRILARLTTTPRTYTSAATAAAANRGHIIKTYFNRDSTTIT
FSMEESSKPVSVCFNNVFLRDASHSAKLVTTGELVHNEKLTAPQDIQISE
DGKSLVVKWKDGGHHQFPLQFFIDYKGSSFVSPATRKQESRVRPQLWNKR
ILKDNVKDLLSVSYNEFIDPKDDSKLFQTLVNLQKFGIAFISGTPSSSSE
GLTIQKICERIGPIRSTVHGEGTFDVNASQATSVNAHYANKDLPLHTDLP
FLENVPGFQILQSLPATEGEDPNTRPMNYFVDAFYATRNVRESDFEAYEA
LQIVPVNYIYENGDKRYYQSKPLIEHHDINEDNTLLGNYEALIKCINYSP
PYQAFFTFGIYDKPSDLNNNLDLNLITTPAKLTERFLFKSFIRGLNLFES
HINDFNNQFRLQLPENCCVIFNNRRILHANSLTSSNQQWLKGCYFDSDTF
KSKLKFLEEKFPHDK

YKL054C, 2717 bp, CDS: 501-2717 (SEQ ID NO 237)
CCTGCTCTAGACGAAGCTAGGGAGGAGGCGCCGTTTGAAAATGGCGGCAA
ACTAAAAGAAGTTGACAAATGAAGTATATATTTTAGCACAGAATGTGCAT
TATTCAACATGTAAATACTAATACTGCAATATCGACTTATAATAATGTAT
AGTGATCCGTATATTAATAGATCTGTTTCAATTCTTTACCTTTTTAGGAT
ATCCGTCACCCGTGATTCCGTCGGAGGTGAGCACTCGCCCAAATAAATAA
CGGGAAATGGTGGCAAAAAGTAGTGGCGGGAAAAGGAAAAATTTTCGTTC
TCTCCCATATAAACGTTTCATTCCTTTTCCTAAGTCTTTTACAGTAATTT
CAGAAACATTCGTATTTTATATTTGATCTTTTGAAGCTACAAGAAAAACT
CTTACCAATTACCCCAAAAAAATCACCATCATAAAGTACTTACATATTTA
TTTTTGTTTGGTCGTTTTCTCAATATAATCTACATCATCATATATATATA
ATGTCTACACAATTTAGGAAGTCTAATCATAATAGTCATAGTAGTAAAAA
ACTAAATCCTGCGCTAAAGTCCAAAATAGATACGCTTACAGAATTGTTCC
CTGACTGGACGAGTGATGATTTAATTGATATAGTTCAAGAATATGATGAT
TTGGAAACTATAATTGATAAAATTACTTCCGGCGCAGTGACAAGATGGGA
TGAAGTAAAGAAACCTGCTAAGAAGGAAAAATATGAAAAAAAGGAGCAAC
AACACTCATATGTCCCTCAACAACATTTGCCAAATCCAGAAGATGATATT
ACATATAAGAGTTCTAATAATAGCAATTCTTTTACTTCTACAAAGCATAA

CAGTAGTAACAATTATACTCAAGCCAGAAATAAGAAGAAGGTACAAACAC
CACGAGCTCATACAACCGGGAAACATGTTAATCTCGACAAGGGGAAGCAC
GTACCATCCAAGCCTGTTTCAAACACTACATCGTGGGCAGCAGCTGTTTC
TGTAGATACTAAACATGACGTTCCTCAAGATTCAAATGATAACAATAATG
AAGAATTAGAAGCACAAGGGCAACAAGCGCAGGAGAAAAATCAAGAAAAA
GAGCAAGAAGAGCAACAACAGCAGGAAGGGCATAATAACAAAGAAGAACA
CAAACAAATAGAGCAACCTTCTTTATCTTCAAAGAAAACAACTTCTAGGA
CATCTGCTTCACAACCAAAGAAAATGTCGTGGGCTGCAATTGCTACACCA
AAGCCAAAGGCTGTTAAAAAGACCGAGTCTCCTCTTGAAAACGTTGCTGA
ATTGAAGAAAGAAATAAGCGATATTAAGAAGGATGACCAAAAGTCTGAAG
CTAGTGAAGAAAAAGTTAATGAACAAGAAACATCTGCACAAGAACAAGAG
GAGGAGACTGCTGAACCTTCTGAAGAAAATGAAGACAGAGTCCCTGAAGT
GGACCGAGAAGAAGTCCAAGAAGAAGCTGAAAAAAAGGAACAAGTAAAAG
AAGAGGAACAGACAGCGGAAGAGCTGGAACAAGAACAAGATAATGTTGCT
GCTCCAGAAGAAGAAGTTACAGTTGTTGAAGAAAAGGTTGAAATTAGTGC
TGTTATTTCAGAGCCTCCAGAAGATCAAGCTAATACTGTACCTCAACCAC
AACAACAATCCCAACAACCACAGCAACCACAGCAACCACAGCAACCACAG
CAACCACAGCAACCACAGCAACAACAACCACAGCAACCACAACAACC
ACAACAACAACTACAACAGCAACAGCAACAGCAACAACAACCAGTACAAG
CTCAAGCTCAAGCCCAAGAAGAACAATTATCTCAAAACTACTATACTCAA
CAACAGCAGCAACAATACGCTCAACAACAGCATCAGTTACAGCAACAGTA
TTTGTCCCAACAACAACAATATGCTCAGCAACAGCAACAGCATCCACAAC
CTCAATCACAACAACCTCAATCACAGCAAAGTCCACAAAGTCAAAAACAA
GGGAACAACGTGGCTGCCCAACAGTACTACATGTATCAAAACCAATTTCC
TGGATATTCTTATCCAGGTATGTTTGATTCACAAGGATACGCTTACGGTC
AACAATATCAGCAACTTGCTCAAAACAACGCTCAAACTAGTGGTAATGCT
AACCAATATAATTTCCAACAAGGTTATGGTCAAGCAGGCGCAACACTGC
TGCTGCTAATTTGACTAGTGCTGCCGCTGCTGCTGCCGCTTCTCCAGCTA
CAGCTCACGCCCAACCTCAACAACAACAGCCATACGGTGGCTCATTCATG
CCATACTACGCCCACTTTTACCAACAGTCATTCCCATATGGTCAACCCTCA
ATACCGGTGTAGCTGGTCAATATCCATACCAGTTACCAAAGAACAATTACA
ACTATTACCAAACTCAAAACGGTCAGGAACAGCAAAGTCCAAATCAAGGT
GTTGCCCAGCATTCTGAAGACTCTCAACAGAAGCAATCACAACAGCAACA
GCAACAGCAACCTCAAGGTCAACCCCAACCTGAAGTTCAAATGCAAAATG
GCCAACCTGTTAACCCACAACAACAAATGCAGTTCCAACAATACTATCAA
TTCCAACAACAACAGCAACAAGCTGCTGCCGCTGCCGCTGCTGCTCCCA
ACAAGGTGTACCATATGGCTACAACGGTTATGATTACAATTCTAAAAATT
CAAGAGGTTTCTACTAA

YKL054C, 738 aa (SEQ ID NO 238)
MSTQFRKSNHNSHSSKKLNPALKSKIDTLTELFPDWTSDDLIDIVQEYDD
LETIIDKITSGAVTRWDEVKKPAKKEKYEKKEQQHSYVPQQHLPNPEDDI
TYKSSNNSNSFTSTKHNSSNNYTQARNKKKVQTPRAHTTGKHVNLDKGKH
VPSKPVSNTTSWAAAVSVDTKHDVPQDSNDNNNEELEAQGQQAQEKNQEK
EQEEQQQQEGHNNKEEHKQIEQPSLSSKKTTSRTSASQPKKMSWAAIATP
KPKAVKKTESPLENVAELKKEISDIKKDDQKSEASEEKVNEQETSAQEQE
EETAEPSEENEDRVPEVDGEEVQEEAEKKEQVKEEEQTAEELEQEQDNVA
APEEEVTVVEEKVEISAVISEPPEDQANTVPQPQQQSQQPQQPQQPQQPQ
QPQQPQQQQQPQQPQQPQQQLQQQQQQQQQPVQAQAQAQEEQLSQNYYTQ
QQQQQYAQQQHQLQQQYLSQQQQYAQQQQQHPQPQSQQPQSQQSPQSQKQ
GNNVAAQQYYMYQNQFPGYSYPGMFDSQGYAYGQQYQQLAQNNAQTSGNA
NQYNFQQGYGQAGANTAAANLTSAAAAAAASPATAHAQPQQQQPYGGSFM
PYYAHFYQQSFPYGQPQYGVAGQYPYQLPKNNYNYYQTQNGQEQQSPNQG
VAQHSEDSQQKQSQQQQQQQPQGQPQPEVQMQNGQPVNPQQQMQFQQYYQ
FQQQQQQAAAAAAAAAQQGVPYGYNGYDYNSKNSRGFY

YLR311C, 848 bp, CDS: 501-848 (SEQ ID NO 283)
ACAAAACAGACTTAGTTATTTTATGGTATACAACAAAAGCTCGAATGAAA
GACGGTTGGCACAAGAGAATTAACAAAATAAACGGAGGAAGAATAAAGTT
ACACCTATTTCTCAAGAATTCTTTTAAATCCGCTCAAGAAAGTTTAAGGG
TATTGCATAAAGAACAGAAACGCCGCTGGAAAAGGCTCTTTGTGCTACTT
CATAATAAATACAGGCAATTTTCTCCACATATTAAAAGGTATTTCGATCA
TTCTTGCCAAAAAGCAAAACAATGTTGGTCGGGATCCAGATTGCAGTTGC
GCAAGCTTCGTTTCAAGTCAATGAAACCATTCCGAGTTTTTCAGTTTAAG
GTTCGCAAAGATACCAACTGGTTTGTAAAGCAGCTGAAACGGTTCGGATT
GAAATTACAGCATTCGAGGATGTATAAAGCGATGTCAGAATGCAGGAAAA
AAAATTATTTTAAGTGCAAACACTAGATCATCCAAAACCCAGCATGAAGA
ATGAAATTAACAAAAGAAAAAAAAAACGACTGCTTAGTAGGAGTGTCATA
TATCCCTCCTTTAAATTTTTTTACACTTACTTTCCTTTTTTTATTGAGAA
TAGAAAAGGTGCATCTCTCTCTCTCTCTCTCTATCTCTATCTCTAAGG
TTTTATTACTTTCATAACGTATGCTATCCATCTCTTTTCCTTTTTTTTTG
TTTTGTTATTCCCTTTTTTTACTCAGTTAGATTCATACTACTATATTTAC
ATATTCTTCGAAGCTTTTATGAGTTAAATATTTTGTTGCTTTATGGGGCA
GAAAATAGTCGACGTCAGTCACCTCCAGGTTATTATGTAATTCGCTAA

YLR311C, 115 aa (SEQ ID NO 284)
MKLTKEKKNDCLVGVSYIPPLNFFTLTFLFLLRIEKVHLSLSLSLSLSLR
FYYFHNVCYPSLFLPFCFVIPFFYSVRFILLYLHILRSFYELNILLLYGA
ENSRRQSPPGYYVIR

YMR107W, 848 bp, CDS: 501-848 (SEQ ID NO 309)
AGAGCAGAAATGATGAAGGGTGTTAGCGCCGTCCACTGATGTGCCTGGTA
GTCATGATTTACGTATAACTAACACATCATGAGGACGGCGGCGGTCACCCC
AACGCAAAAGAGTGACTTCCCTGCGCTTTGCCAAAACCCCATACATCGCC
ATCTGGCTCCTGGCAGGGCGGTTGATGGACATCAGCCGCCTCCCTTAATT
GCTAAAGCCTCCACAAGGCACAATTAAGCAATATTTCGGGAAAGTACACC
AGTCAGTTTGCGCTTTTATGACTGGGTTCTAAGGTACTAGATGTGAAGTA
GTGGTGACAGAATCAGGGAGATAAGAGGGAGCAGGGTGGGGTAATGATGT
GCGATAACAATCTTGCTTGGCTAATCACCCCCATATCTTGTAGTGAGTAT
ATAAATAGGAGCCTCCCTTCCTATTGCAACTCCATAAAATTTTTTTTTGT
AGCCACTTCTGTAACAAGATAAATAAAACCAACTAATCGAGATATCAAAT
ATGGGTAGTTTTTGGGACGCATTCGCAGTATACGACAAGAAAAAGCACGC
AGATCCAAGTGTATATGGAGGAAACCATAACAACACAGGAGACAGTAAAA
CGCAGGTTATGTTTTCGAAAGAGTACCGTCAACCTAGGACACATCAGCAA
GAGAACTTGCAGAGCATGAGAAGATCTTCCATAGGATCACAGGACAGTTC
CGATGTTGAGGACGTTAAGGAAGGGAGATTACCCGCAGAAGTAGAAATAC
CAAAGAATGTTGACATCTCTAACATGTCGCAAGGTGAGTTTTTAAGACTT
TACGAAAGTTTGAGGAGGGGGGAACCCGACAATAAAGTAAATAGATAA

YMR107W, 115 aa (SEQ ID NO 310)
MGSFWDAFAVYDKKKHADPSVYGGNHNNTGDSKTQVMFSKEYRQPRTHQQ
ENLQSMRRSSIGSQDSSDVEDVKEGRLPAEVEIPKNVDISNMSQGEFLRL
YESLRRGEPDNKVNR

YKL066W, 944 bp, CDS: 501-944 (SEQ ID NO 243)
GAAAAACATCTCATAAATCATCCCTGGAAAAATGTCTAGTCAAACAGAAA
GAACTTTTATTGCGGTAAAACCAGATGGTGTCCAGAGGGGCTTAGTATCT
CAAATTCTATCTCGTTTTGAAAAAAAAGGTTACAAACTAGTTGCTATTAA
ATTAGTTAAAGCGGATGATAAATTACTAGAGCAACATTACGCAGAGCATG
TTGGTAAACCATTTTTCCCAAAGATGGTATCCTTTATGAAGTCTGGTCCC
ATTTTGGCCACGGTCTGGGAGGGAAAAGATGTGGTTAGACAAGGAAGAAC
TATTCTTGGTGCTACTAATCCTTTGGGCAGTGCACCAGGTACCATTAGAG

GTGATTTCGGTATTGACCTAGGCAGAAACGTCTGTCACGGCAGTGATTCT
GTTGATAGCGCTGAACGTGAAATCAATTTGTGGTTTAAGAAGGAAGAGTT
AGTTGATTGGGAATCTAATCAAGCTAAGTGGATTTATGAATGAATAACTT
ATGGCATGGGAGGGTACATATGAGCGCCTTTTTTTTCTCGCTTTGGGCAG
CTCATATCATGTTCCCTCACTAGCTAATAATATAATGAATTTTTTAGAAG
GAGCACGATTATATAAAAAAAATACCACTTATGTTGCTACCCTTATATAC
GAATTTATAATACTTAATGACGCTTCAATGACGCCTGATGTCAAATGCTT
TTGGCTCCCAGTGAAATTGCCACACTTCCTTCTTCTTTCCGAACTTTATA
GTATCATCGAAAAATACAAGTTGGCAAAGGTCTATTACAATCGCGGAACG
TACGATGTTCATACGGTTTCAGCGAATAGTCTTGTAATATCCGGAAGCAT
GCCTACCGGCATTATTATAGGTAGTTCATCGCCCTTGGACTATGTAGGGG
TACAAGTAAATAGGCAACTTGAAATGGATCTCCCTATTGAATGA

YKL066W, 147 aa (SEQ ID NO 244)
MAWEGTYERLFFLALGSSYHVPSLANNIMNFLEGARLYKKNTTYVATLIY
EFIILNDASMTPDVKCFWLPVKLPHFLLLSELYSIIEKYKLAKVYYNRGT
YDVHTVSANSLVISGSSMPTGIIIGSSSPLDYVGVQVNRQLEMDLPIE

YML053C, 1139 bp, CDS: 501-1139 (SEQ ID NO 295)
GAGGCGACACCTGCTAATGTTTACAATTTTCCCGATTGGGGTGCTAGAGG
CATACAGTGGGCTACATGGCACAGCACGGCAGTGCAGAGTGAGAAAATAT
GACTTCACGCTCGAGGCGAGGCCACGCTTTCGAAGCTTCGAATGCCTCACTA
CCTAGACCATTGCTGTTTTGTACCTTCACGGTCCCATTAGAGACATTTTA
CTTAATGCAAGATTGCCATATCCGTTGTCATGGTACCAAACAGGGTAATA
ATTTCTAGAAATCATGATACACGTATGACATCTGGGTAACCTAATCCATC
TGGGTAACCGATTTTTCTCTCCCTTTGCTTTCTCTTTACCACTCAGCTGA
CTTTATTATTTTTTTTATATTTTTCATTTTGACAAAATTATATAGTTAGG
AAGAATACAATAGGACTGCGACAGAAACAGATAAGGGCTCTTTTTTCTTG
GGGTTGGCTGCTTTTATTCATTAATTTAAGACTCAAGTGTGCTGCGTGAA
ATGCTCTCATACTATGAACACAATACTGCGTTCCAAACAAACAATTGCAA
TTCCGGTAGCAATGCCGCCACTACATACAACAGCGACGCCAATAATGATA
CGATCATGAATAAAAGAAAAAATGACCATTTCGAGTTTGATACACACACT
TTCTACCAAAGATCGAAGAGAACAAAACGAGATTCTGTAAGTACAAAGTT
TTCGGTCGGTTCCGGGTGTGCTAATCTTAATAACAACAACAACAACATCA
TCATCAACAACAACAACAACAACAATAATAATAATAATAACCATAATCAT
AATAACAGCAATAATACTGCAACCTACAATAATATTCATTATAAAAAAAA
TATCGAAATATGTCCCCTGAAACCGGTTAGTATGCACCACACTATGAACA
GCCGCTTACTGAACGAATCTGAATTTTATTCTGAAACAGAAGAGTACATG
ATTCATGGTTATTTCGGTAACACTAATCGCGACATAACAGGCACGAGTCC
TACTGGAAGTGCTAGTATTATACAACACCAGTATCATCTTCTACCATCCC
AAAGTATAATTGCATCACAAGCACCCGGTACTGCCATGGCCGCGTTGACT
AACAACAATATCGCTAACGATTACATGGATATAGATTAA

YML053C, 212 aa (SEQ ID NO 296)
MLSYYEHNTAFQTNNCNSGSNAATTYNSDANNDTIMNKRKNDHFEFDTHT
FYQRSKRTKRDSVSTKFSVGSGCANLNNNNNNIIINNNNNNNNNNNNNHH
NNSNNTATYNNIHYKKNIEICPLKPVSMHHTMNSRLLNESEPYSETEEYM
IHGYFGNTNRDITGTSPTGSASIIQHQYHLLPSQSIIASQAPGTAMAALT
NNNIANDYMDID

YOR121C, 806 bp, CDS: 501-806 (SEQ ID NO 355)
GGTGACGCTGTTTGGGCTACTTCTGGTGGCCTATCTTTGCAACCAAACGA
AATTGGTGAAATTGTTCAAGGCTTCGACAATCCAGCTGGTTTGCAAAGCA
ATGGTTTGCATATTCAAGGCCAAAAGTTCATGTTGTTGAGAGCTGACGAT
AGAAGTATCTACGGTAGACATGATGCTGAGGGTGTTGTTTGTTGTAAGAAC
TAAGCAAACCGTTATTATTGCTCATTATCCACCAACCGTACAAGCCGGTG

AGGCCACCAAGATTGTCGAGCAATTGGCTGACTACTTGATTGGTGTTCAA
TACTAATTTATGCAGGTAAAGTTTTCTTGCCTTATACACCACCTATTCTG
GCATCTGCGGGATTTCGCTTCCTATTTTACAAATATTTTATTGATTGACG
CTAATTATCACTGTAAAAGGCGCACTTTTATATGTAGTCACATCCGGTA
TTTAACATATTTACGAAACAGTCTTAAGAATATCGACATTTGATATACTT
ATGTTTAATTTATCTACATATTACAATCATACGAGAAACACGCAAAAACA
ATTACTTGAATACTTCGAAAGGAGACCAATTTGGATGTACAACCCTTTTT
TCGCCCTTTTCCTTCGATATGTTATTGATAGCTTCAAAGTCCTCAGTAGA
CAAAGTAAATATTTTCCTGTTCGTTTTGATTCGATCGGGATTCACAGATT
TTGGCAAGACAACATAACCTCTTTGGACGTGCCAGCTAATAACAACGTGT
CCGGGTTGAACGTTATTTTTCTTCGCAATTTCAAGGATAACCGGTTCCTT
CAATAG

YOR121C, 101 aa (SEQ ID NO 356)
MFNLSTYYNHTRNTQKQLLEYFERRPIWMYNPFFALFLRYVIDSFKVLSR
QSKYFPVRFDSIGIHRFWQDNITSLDVPANNNVSGLNVIFLRNFKDNRFL
Q

YOL106W, 854 bp, CDS: 501-854 (SEQ ID NO 341)
ATATGGTTTCATCATTTTGCTCAATTGTCTCCATTTGGGTTACCTTTTT
TGCCAGTTGGTCGTACTTGAGGTTTTTCCAGAAACTTGCACCCTTGAATT
GTCCCTCTTTGCCAACAACTAATTCTCAAGGTGGTCAGGAAATATTGGTC
GGCGATGCATCTGATACTTTTCAATTGATTTACTTCTTTCCTGATCTAAT
TAAGCCGATTTTGAGGCCGATTTTCAATTTCATTTATAATGTAGTTGTTG
TAAAATTTAAAGTCATTAAACCTTTTCATGATATTGATATAGATATTGGG
AACACCATCGCAGAAAGTAGAGGCGCCAAAAAAAATTATGACTGTAGAAGA
AAGACGAAGACAGTTAGCTTTACAAGTTTTGGAAGAGCGTATGGTAAACC
CTTGATATATGGATCTATATAACTTGAAATATGCTCTATTATATCGTGAT
TTAATGACGGCTGTTGGCATTTCGGTCTTTACCAAGGTAGTAGGATTTGT
ATGCTGAATGTGCGCCAGTACTATCGAACCATAGAAACCCATATATTCCC
CAATATTAATAATTCTACTGAGAAATGGGTGAATTTTGAAATAATTGTTG
GGATTCCATCGTTGATAAAGGCTATAATATTAGGTATACAGAATGTACTA
GAAGTTCTCCTCGATGATATAGGAATCCCCATAATGGAATCTATATTTCT
ATGTACCAATATTACGATTATTCCTCATTCCATTTCATATGTTTCATTAT
CCTATTACATTATCGATCCTTGCATTTCAGCTTCCTCTAACTTCGGTGAC
AGCTTCTATAATAACTTATGTCACTATCTAACACCGTATATGATAATATA
TTGA

YOL106W, 117 aa (SEQ ID NO 342)
MLNVRQYYRTIETHIFPNINNSTEKWVNFEIIVGIPSLIKAIILGIQNVL
EVLLDDIGIPIMESIFLCTNITIIPHSISYVSLSYYIIDPCISASSNFGD
SFYNNLCHYLTPYMIIY

>YAL003W, 1487 bp, exon1: 501-580, intron1: 581-946, exon2:
947-1487 (SEQ ID NO 17)
CCGATGGAACGTTCTGGAAAAAGAAGAATAATTTAATTACTTTCTCAACTAAAATCTGGA
GAAAAAACGCAAATGACAGCTTCTAAACGTTCCGTGTGCTTTCTTTCTAGAATGTTCTGG
AAAGTTTACAACAATCCACACAAGAACGAAAATGCCGTTGACAATGATGAAACCATCATCCA
CACACCGCGCACACGTGCTTTATTTCTTTTTCTGAATTTTTTTTTTCCGCCATTTTCAAC
CAAGGAAATTTTTTTTCTTAGGGCTCAGAACCTGCAGGTGAAGAAGCGCTTTAGAAATCA
AAGCACAACGTAACAATTTGTCGACAACCGAGCCTTTGAAGAAAAAATTTTTCACATTGT
CGCCTCTAAATAAATAGTTTAAGGTTATCTACCCACTATATTTAGTTGGTTCTTTTTTTT
TTCCTTCTACTCTTTATCTTTTTACCTCATGCTTTCTACCTTTCAGCACTGAAGAGTCCA
ACCGAATATATACACACATAATGGCATCCACCGATTTCTCCAAGATTGAAACTTTGAAAC
AATTAAACGCTTCTTTGGCTGACAAGTCATACATTGAAGGGTATGTTCCGATTTAGTTTA

CTTTATAGATCGTTGTTTTTCTTTCTTTTTTTTTTTTCCTATGGTTACATGTAAAGGGAA
GTTAACTAATAATGATTACTTTTTTTCGCTTATGTGAATGATGAATTTAATTCTTTGGTC
CGTGTTTATGATGGGAAGTAAGACCCCCGATATGAGTGACAAAAGAGATGTGGTTGACTA
TCACAGTATCTGACGATAGCACAGAGCAGAGTATCATTATTAGTTATCTGTTATTTTTTT
TTCCTTTTTTGTTCAAAAAAAGAAAGACAGAGTCTAAAGATTGCATTACAAGAAAAAGT
TCTCATTACTAACAAGCAAAATGTTTTGTTTCTCCTTTTAAAATAGTACTGCTGTTTCTC
AAGCTGACGTCACTGTCTTCAAGGCTTTCCAATCTGCTTACCCAGAATTCTCCAGATGGT
TCAACCACATCGCTTCCAAGGCCGATGAATTCGACTCTTTCCCAGCTGCCTCTGCTGCCG
CTGCCGAAGAAGAAGAAGATGACGATGTCGATTTATTCGGTTCCGACGATGAAGAAGCTG
ACGCTGAAGCTGAAAAGTTGAAGGCTGAAAGAATTGCCGCATACAACGCTAAGAAGGCTG
CTAAGCCAGCTAAGCCAGCTGCTAAGTCCATTGTCACTCTAGATGTCAAGCCATGGGATG
ATGAAACCAATTTGGAAGAAATGGTTGCTAACGTCAAGGCCATCGAAATGGAAGGTTTGA
CCTGGGGTGCTCACCAATTTATCCCAATTGGTTTCGGTATCAAGAAGTTGCAAATTAACT
GTGTTGTCGAAGATGACAAGGTTTCCTTGGATGACTTGCAACAAAGCATTGAAGAAGACG
AAGACCACGTCCAATCTACCGATATTGCTGCTATGCAAAAATTATAA

>YAL003W, 206 aa (SEQ ID NO 18)
MASTDFSKIETLKQLNASLADKSYIEGTAVSQADVTVFKAFQSAYPEFSRWFNHIASKAD
EFDSFPAASAAAAEEEEDDDVDLFGSDDEEADAEAEKLKAERIAAYNAKKAAKPAKPAAK
SIVTLDVKPWDDETNLEEMVANVKAIEMEGLTWGAHQFIPIGFGIKKLQINCVVEDDKVS
LDDLQQSIEEDEDHVQSTDIAAMQKL

>YAL060W, 1649 bp, CDS: 501-1649 (SEQ ID NO 19)
AAAGACTACGAGAATCAATAAACGAGGCTAAACTGCGTCACACATGATTGTGATTGAGTA
CTCACGTTCTCGTGTTAATCCCGCGGTCTTCTTGTTTACTAACTTTTCTTTCTCTCATA
GCATTCTCTTGACAGTGTTTTATATACATCATATGTACATTTATCGAGCCAATCGAGGGC
AGCAGTTTAACATCAAGCCGGATTTGCTCACGCTACTTTGACCCCTTTTCGTTTCGACGG
AGAGAAGAAACCGGTGTTTTCCTATCCTTGCCTATTCTTTCCTCCTTACGGGGTCCTAGC
CTGTTTCTCTTGATATGATAATAGGTGGAAACGTAGAAAAAAAAATCGACATATAAAAGT
GGGGCAGATACTTCGTGTGACAATGGCCAATTCAAGCCCTTTGGGCAGATGTTGCCCTTC
TTCTTTCTTAAAAAGTCTTAGTACGATTGACCAAGTCAGAAAAAAAAAAAAAAAAGGAACT
AAAAAAAGTTTTAATTAATTATGAGAGCTTTGGCATATTTCAAGAAGGGTGATATTCACT
TCACTAATGATATCCCTAGGCCAGAAATCCAAACCGACGATGAGGTTATTATCGACGTCT
CTTGGTGTGGGATTTGTGGCTCGGATCTTCACGAGTACTTGGATGGTCCAATCTTCATGC
CTAAAGATGGAGAGTGCCATAAATTATCCAACGCTGCTTTACCTCTGGCAATGGGCCATG
AGATGTCAGGAATTGTTTCCAAGGTTGGTCCTAAAGTGACAAAGGTGAAGGTTGGCGACC
ACGTGGTCGTTGATGCTGCCAGCAGTTGTGCGGACCTGCATTGCTGGCCACACTCCAAAT
TTTACAATTCCAAACCATGTGATGCTTGTCAGAGGGCAGTGAAAATCTATGTACCCACG
CCGGTTTTGTAGGACTAGGTGTGATCAGTGGTGGCTTTGCTGAACAAGTCGTAGTCTCTC
AACATCACATTATCCCGGTTCCAAAGGAAATTCCTCTAGATGTGGCTGCTTTAGTTGAGC
CTCTTTCTGTCACCTGGCATGCTGTTAAGATTTCTGGTTTCAAAAAAGGCAGTTCAGCCT
TGGTTCTTGGTGCAGGTCCCATTGGGTTGTGTACCATTTTGGTACTTAAGGGAATGGGGG
CTAGTAAAATTGTAGTGTCTGAAATTGCAGAGAGAAGAATAGAAATGGCCAAGAAACTGG
GCGTTGAGGTGTTCAATCCCTCCAAGCACGGTCATAAATCTATAGAGATACTACGTGGTT
TGACCAAGAGCCATGATGGGTTTGATTACAGTTATGATTGTTCTGGTATTCAAGTTACTT
TCGAAACCTCTTTGAAGGCATTAACATTCAAGGGGACAGCCACCAACATTGCAGTTTGGG
GTCCAAAACCTGTCCCATTCCAACCAATGGATGTGACTCTCCAAGAGAAGTTATGACTG
GTTCGATCGGCTATGTTGTCGAAGCCTTCGAAGAAGTTGTTCGTGCCATCCACAACGGAG
ACATCGCCATGGAAGATTGTAAGCAACTAATCACTGGTAAGCAAAGGATTGAGGACGGTT
GGGAAAAGGGATTCCAAGAGTTGATGGATCACAAGGAATCCAACGTTAAGATTCTATTGA
CGCCTAACAATCACGGTGAAATGAAGTAA

>YAL060W, 382 aa (SEQ ID NO 20)
MRALAYFKKGDIHFTNDIPRPEIQTDDEVIIDVSWCGICGSDLHEYLDGPIFMPKDGECH
KLSNAALPLAMGHEMSGIVSKVGPKVTKVKVGDHVVVDAASSCADLHCWPHSKFYNSKPC
DACQRGSENLCTHAGFVGLGVISGGFAEQVVVSQHHIIPVPKEIPLDVAALVEPLSVTWH

AVKISGFKKGSSALVLGAGPIGLCTILVLKGMGASKIVVSEIAERRIEMAKKLGVEVFNP
SKHGHKSIEILRGLTKSHDGFDYSYDCSGIQVTFETSLKALTFKGTATNIAVWGPKPVPF
QPMDVTLQEKVMTGSIGYVVEAFEEVVRAIHNGDIAMEDCKQLITGKQRIEDGWEKGFQE
LMDHKESNVKILLTPNNHGEMK

>YBL058W, 1772 bp, CDS: 501-1772 (SEQ ID NO 23)
TTATTTACATAGTGCCATTGAACACTTTTCAAGCAAACTACGCCAGCCGGACGCAGACAA
TAACACACACACAAAAGAGTCTTGCAGGTTCTCTTTTAGCGGCAACGGGCATGACACTAG
GTATATTTGGTATGGGCATCACAGGGACATGTTGGAGCTGGGATGTTTCATCATTTCAGG
AACTAAAGCAACGTCTGGAAAGGCGTGCCAACAACGAATTTGTAGTGACAAACATGCCTC
TGGATAAAAGAAGCCAGCAAGTAGTGGACAGCTTAGTTAAGACACACAATTCATCTCTTT
GTAAATAGTGTTATACCATAGTAGTAGTTTCAATAATATATTCCACTACTTATATGTGTT
ACCCGCATTAGAACTCTTATTGGTGGCGAAAATCGATGGCAATAAAGAACGGAAGGGGTT
TAATAGTTGTATGCTTAACATATTTCGATTTAAATATATAAGAAACGTCGGTAGCACAAC
AATTAACTCATTATTTAGGTATGGCGGAAATACCTGATGAAACCATCCAGCAGTTCATGG
CATTGACCAATGTGTCGCATAACATAGCCGTTCAATATCTCTCTGAATTTGGAGATTTAA
ATGAAGCACTAAATTCCTATTATGCTTCTCAAACGGATGACCAAAAGGATAGAAGAGAGG
AAGCACATTGGAACAGACAGGAGAAGGCCCTCAAGCAAGAAGCCTTCTCCACCAACT
CTTCGAATAAAGCCATAAATACGGAGCACGTTGGTGGGTTATGTCCAAAACCAGGATCCT
CACAAGGTAGCAACGAGTACTTGAAAAGGAAAGGTTCTACCTCTCCTGAACCAACCAAGG
GTAGTAGCCGCTCTGGAAGTGGTAACAACTCCAGGTTTATGAGCTTTTCGGATATGGTAA
GAGGTCAAGCTGATGATGACGATGAAGATCAACCCAGAAATACTTTTGCTGGTGGTGAAA
CATCCGGCTTAGAGGTTACAGATCCTTCAGATCCTAATTCATTACTGAAGGATTTGCTGG
AAAAAGCGAGAAGGGGTGGTCAAATGGGCGCTGAAAACGGATTCCGTGATGACGAAGACC
ATGAAATGGGTGCCAATAGGTTTACTGGAAGAGGTTTAGATTAGGGTCAACCATCGACG
CAGCAGATGAAGTCGTAGAAGACAACACTTCACAATCACAACGTAGACCAGAAAAAGTCA
CAAGAGAAATTACATTTTGGAAGGAAGGTTTTCAAGTGGCCGATGGTCCGCTTTATCGCT
ATGATGATCCTGCGAACAGTTTCTATTTGAGCGAGTTAAATCAAGGGAGGGCTCCATTAA
AGCTCTTAGATGTGCAATTTGGACAAGAAGTTGAAGTTAATGTATATAAAAAATTAGATG
AGTCTTATAAAGCTCCGACGAGAAAACTGGGCGGTTTTCAGGCCAGGGCCAAAGACTAG
GATCTCCTATCCCGGGTGAATCGTCACCTGCGGAGGTTCCAAAGAATGAGACACCCGCTG
CTCAGGAACAACCCATGCCGGACAATGAGCCAAAACAAGGCGACACCTCCATCCAAATTA
GATACGCAAATGGCAAAAGAGAAGTTTTGCACTGCAATTCCACAGATACAGTAAAGTTTT
TGTATGAGCATGTGACATCAAATGCGAACACTGACCCATCGAGGAATTTCACCTTGAATT
ATGCCTTTCCTATCAAACCAATAAGCAACGATGAGACAACATTGAAGGACGCTGATCTGC
TGAACTCCGTTGTCGTGCAAAGATGGGCATGA

>YBL058W, 423 aa (SEQ ID NO 24)
MAEIPDETIQQFMALTNVSHNIAVQYLSEPGDLNEALNSYYASQTDDQKDRREEAHWNRQ
QEKALKQEAFSTNSSNKAINTEHVGGLCPKPGSSQGSNEYLKRKGSTSPEPTKGSSRSGS
GNNSRFMSFSDMVRGQADDDDEDQPRNTFAGGETSGLEVTDPSDPNSLLKDLLEKARRGG
QMGAENGFRDDEDHEMGANRFTGRGFRLGSTIDAADEVVEDNTSQSQRRPEKVTREITFW
KEGFQVADGPLYRYDDPANSFYLSELNQGRAPLKLLDVQFGQEVEVNVYKKLDESYKAPT
RKLGGFSGQGQRLGSPIPGESSPAEVPKNETPAAQEQPMPDNEPKQGDTSIQIRYANGKR
EVLHCNSTDTVKFLYEHVTSNANTDPSRNFTLNYAFPIKPISNDETTLKDADLLNSVVVQ
RWA

>YBR039W, 1436 bp, CDS: 501-1436 (SEQ ID NO 41)
TTGAGATTTTCCAAGTAGTAACTCATCTTTCTGAGTGTGCTATCAAATACATACTAAGGA
GAATAAACTCTTGTTATTACGTATTCTTCATCCTTATGGGTAGAGAGCGCACTGTTTTAG
TACATTTTCTAGACGTCGAAACGTAGAGCAATTGTCGATAAAACAAAAAAAAAGTAAGAA
GATATATGAATAGGACGTGTCGCTAGAACTAGTAAGTATATGATGGAGATATAATAAGTG
AATTATTCGATATTTAATGAACGTTCTCATTTATTTGGAAGAAATGTTTATCACGTGATG
GAGAACCAATGAGCGGCGAGTAACTACGCGAGGAACCCGGACCGCAATAACGATTAAAGA
AGGCCCGGAAGGGAGATGCTTAAATGATTATCACTCAGTTAAAAAAGACAAATAAGAAAC
TATTGAGACTGAACCGTTTTGGTTAATTTCAGGTGGAAACAATTGAAGACGAGCAGTAAA

CATTATTTTATTTAGTAGTCATGTTGTCAAGAATTGTATCAAACAATGCAACACGCTCCG
TAATGTGCCACCAAGCGCAAGTGGGTATTCTTTATAAGACTAACCCAGTGAGAACTTATG
CTACTTTGAAAGAAGTGGAAATGCGTTTGAAATCTATCAAAAATATTGAGAAGATCACAA
AAACTATGAAGATTGTTGCATCTACAAGATTGAGTAAAGCTGAAAAGGCTAAAATTTCCG
CAAAGAAGATGGATGAAGCAGAGCAGTTGTTTTACAAGAACGCCGAAACCAAAAATTTGG
ATGTTGAGGCTACTGAAACAGGTGCTCCTAAAGAGTTGATTGTTGCTATCACCTCTGATA
AGGGGTTGTGTGGTTCTATCCACTCTCAATTGGCTAAAGCTGTGAGAAGACATTTGAATG
ATCAACCAAACGCCGATATAGTCACTATTGGTGATAAAATTAAAATGCAGCTATTGAGAA
CCCATCCTAACAACATTAAATTGTCTATTAATGGAATTGGTAAAGATGCCCCAACTTTCC
AAGAATCTGCTTTGATTGCCGATAAGTTATTGAGTGTCATGAAGGCCGGCACTTACCCAA
AGATTTCCATTTTCTACAATGACCCAGTGTCTTCCCTATCTTTTGAACCATCTGAAAAAC
CGATCTTTAACGCCAAGACCATTGAACAATCCCCATCATTCGGCAAATTTGAGATCGACA
CGGACGCAAACGTTCCAAGAGATTTGTTTGAATATACTTTGGCTAACCAAATGTTGACAG
CAATGGCTCAAGGTTATGCTGCTGAAATTTCCGCCAGAAGAAACGCTATGGATAACGCTT
CCAAGAATGCCGGTGATATGATCAATCGTTACTCTATCTTGTACAACAGAACAAGACAAG
CTGTCATTACTAATGAACTGGTTGATATTATTACTGGTGCTTCCTCTTTGGGATGA

>YBR039W, 311 aa (SEQ ID NO 42)
MLSRIVSNNATRSVMCHQAQVGILYKTNPVRTYATLKEVEMRLKSIKNIEKITKTMKIVA
STRLSKAEKAKISAKKMDEAEQLFYKNAETKNLDVEATETGAPKELIVAITSDKGLCGSI
HSQLAKAVRRHLNDQPNADIVTIGDKIKMQLLRTHPNNIKLSINGIGKDAPTFQESALIA
DKLLSVMKAGTYPKISIFYNDPVSSLSFEPSEKPIFNAKTIEQSPSFGKFEIDTDANVPR
DLFEYTLANQMLTAMAQGYAAEISARRNAMDNASKNAGDMINRYSILYNRTRQAVITNEL
VDIITGASSLG

>YBR062C, 848 bp, CDS: 501-848 (SEQ ID NO 45)
CCATTTTGGTGACCAACTCTCCTACCCGAATTACTGTGATGATATATACTCTTCGTTTTC
TAGTAATGGCTTCATTTTGCCTAAGTTGGTCAAAATTGTTGTGGGCGGCTTTTGTTTGCA
CCGAGGAGCGCTCAGTTCGTTATAATACCAGTTTTGCCACTCCTAAACTACTAAAGAAAT
AATAGAAAGATATTATTCATCAAACATAATCACAATCAAAAAAATGTCTACATATGAAGGT
ATGTAATGATATATTATGAAGTAAGTTCCCCAAAGCCAATTAACTAACCGAATTTTAATC
TGCACTCATCATTAGATTAGAGGAACATGGAATACAACAAAACTCAAGGGATTACCAAGA
AGTAGGAGGAACTTCACAGGAGGAGCAGAGAAGACAGGTCAAGATCCCAACTGCAAGGTC
TATTTCAAAACTTTGGTAACACCAGTGGTGAGGGTGATGCACATTCAGATTCAACACTAC
TTTTACGATTATTATCGCAAATGCTTCCAGAATCATTACAGGAAGAATGGTTGCAAGAAA
TGGATAAAGGCAAGAGTGCGGGCTGTCCTGATACTTTTGCAGCCTCTTTACCACGAATCA
ATAAAAAAAAGCTCAAAGCAACTGACAACTGCTCCATTTGTTACACTAATTATTTAGAAG
ATGAGTACCCCTTAGTAGTTGAATTACCTCATTGCCATCATAAGTTCGACTTAGAGTGTT
TGTCTGTCTGGCTATCTCGAAGTACAACATGTCCATTATGCAGAGATAATGTTATGGGCC
ACCGAATCATTAATGAGATTGATACAACTGAAGCAGAACTGGAAGAAGATTGGGGTATGT
ACGGTTAA

>YBR062C, 115 aa (SEQ ID NO 46)
MLPESLQEEWLQEMDKGKSAGCPDTFAASLPRINKKKLKATDNCSICYTNYLEDEYPLVV
ELPHCHHKFDLECLSVWLSRSTTCPLCRDNVMGHRIINEIDTTEAELEEDWGMYG

>YBR101C, 1373 bp, CDS: 501-1373 (SEQ ID NO 49)
AATGATGAAATGTTATCCCCAGGGTCCATTAAGTCATCCAGAAAACAGATAGATGGATTG
AAGGCCGTAGGTTTGGATTTTGTCTACAAATTGGACGAGTTTATCAAAAAGAACAGTGAT
AAAATTCGCTAAACAAGATCACAGAAAATAAACCTCACTTCAATATATATGATGTGTAGG
TAGGGTATATACTTATACCACTGCTGTCGACAGTGTACTAACCTATTTCCTATTTTGTAG
GTAAGCTTTTCAGCTACTGGTTGGTCAAGTTGGGCCCTATTAAGGTTGTAATCAGCTTAT
TCGTTTGAAATGATATACCTCTTGGACTGGAATCTTCTGGAAGTTTTTTGGAGGTTAGAA
AAGAGGAAGGCATCTCGCGCTGACAGAAATTTGCTTATAAACCAGCGATTGGCTATATCT
AAAAGAGCACTCATCGTCAGTCAGAAAGCCATTACCTTTCAACGAAGAGTAAAATAGAA
AAAAAAACACATACATAACTATGGAAAAGCTATTACAGTGGTCTATTGCGAATTCTCAAG

GGGACAAAGAAGCTATGGCTAGGGCCGGCCAACCTGATCCTAAATTGCTACAGCAGTTAT
TCGGTGGTGGTGGTCCTGACGATCCAACCTTAATGAAAGAATCCATGGCTGTTATTATGA
ATCCGGAGGTTGACTTAGAAACAAAACTCGTTGCATTTGACAACTTTGAAATGTTGATTG
AGAACTTAGATAATGCTAATAATATCGAAAATTTAAAACTGTGGGAGCCATTGTTGGATG
TTCTTGTTCAGACGAAGGATGAAGAACTACGTGCTGCTGCTTTATCCATTATTGGAACGG
CTGTGCAAAACAACTTGGATTCGCAAAATAATTTCATGAAATACGACAATGGTCTGCGAA
GCCTTATCGAAATAGCTAGTGACAAGACAAAGCCACTCGACGTGAGAACAAAAGCTTTTT
ACGCACTATCTAATCTAATAAGAAACCACAAAGATATCTCAGAAAAGTTTTTCAAATTAA
ATGGGCTCGACTGCATAGCACCTGTATTAAGTGATAACACCGCCAAACCAAAACTGAAAA
TGAGAGCCATTGCCTTATTGACCGCATATTTGTCATCTGTTAAGATTGATGAAAATATAA
TCAGTGTGCTGAGAAAGGATGGAGTAATTGAAAGTACGATTGAGTGCTTGTCTGACGAGA
GTAACTTGAACATCATAGATAGAGTTCTGTCTTTTCTCTCTCACCTGATATCTTCCGGAA
TAAAATTTAATGAACAGGAATTGCACAAATTGAACGAAGGTTACAAACATATCGAGCCTC
TAAAGGACAGACTTAATGAAGACGATTATTTAGCCGTAAAGTATGTATTATGA

>YBR101C, 290 aa (SEQ ID NO 50)
MEKLLQWSIANSQGDKEAMARAGQPDPKLLQQLFGGGGPDDPTLMKESMAVIMNPEVDLE
TKLVAFDNFEMLIENLDNANNIENLKLWEPLLDVLVQTKDEELRAAALSIIGTAVQNNLD
SQNNFMKYDNGLRSLIEIASDKTKPLDVRTKAFYALSNLIRNHKDISEKFFKLNGLDCIA
PVLSDNTAKPKLKMRAIALLTAYLSSVKIDENIISVLRKDGVIESTIECLSDESNLNIID
RVLSFLSHLISSGIKFNEQELHKLNEGYKHIEPLKDRLNEDDYLAVKYVL

>YBR139W, 2027 bp, CDS: 501-2027 (SEQ ID NO 55)
GGAGGAGTCAAGGGCCTGGAAAGTACGGATCCTGTAGAAATATCACTGGCAATTATACTG
AGTTTATTGTTGGTGTTGCTATTCATATTTGAGCTGGTATTGGACGAAAGCAAGGATAAT
GAGTTTGTGTCTACTGACTCCAACACCCTAGGCTGGATTTGATCTTTCTCCATCCTTTAA
TTTTAACCTTTTAATTAGTGGTTGGATCAAGTTTTCGAGACTATTCCAATCTGTGACTTG
TTGGATAAATAGTTTTTGACTCGTTTAGTATAATCCTTTTTTCTAAAAGTGCTTAGAGTT
CTCTAAGATGTTCTTGTTTACAATGTGAGCGATTTAGGAAATTTCCTAAAAATGGCCGAG
GCGGCGCTAGCATTCTACGAAAGGTGAGATAACGCTTCGTTATCGAAAAATGTCAGGGGA
CAGGGGTTATATAAGAACGAAAATTGTCATCCCTGCATTTTTTCTTTAAAACAGCTATACA
AAAAGTGATACCGACATCAATGAAGTATCTAAACTTAGTTTTCGTGCTTCAGCTTCTTTA
TTAGCATCAAATACGCCTCATTCGGCCGAGCCTTTTCTCTTTTTGAAGATGATACCACCT
TTGCCAATTTGGATAAACAGCTAAAGCTTCCACAGAATACACAGCAAACCCTTAAATTGG
ACCGTTTGAATCACGATGATCCGCTGTTTACAACTTTTATTTCTTCTGTGGACACAGATT
ACAGTTTGAGACTTAGAACAGTAGATCCTTCTAAACTAGGAATTGACACCGTAAAACAAT
GGTCGGGTTACATGGACTATAAGGATTCCAAACACTTTTTTTACTGGTTTTTTGAAAGTA
GGAACGATCCTGCTAACGACCCAATTATTCTTTGGTTAAATGGTGGACCTGGTTGTTCCT
CGTTTACTGGGTTGCTATTTGAACTAGGCCCCTCATCAATTGGCGCCGATATGAAACCAA
TCCACAATCCCTATTCTTGGAATAATAACGCTTCAATGATCTTCTTAGAACAGCCACTCG
GAGTCGGCTTTTCCTATGGTGATGAAAAAGTCTCCTCTACAAAATTAGCAGGCAAAGATG
CGTACATTTTCCTGGAATTGTTTTTTGAAGCTTTTCCTCATTTACGCTCCAACGATTTCC
ACATTGCAGGCGAATCCTATGCAGGACATTATATCCCTCAAATTGCACATGAGATCGTTG
TCAAGAACCCTGAAAGAACGTTCAATTTAACTTCAGTTATGATTGGTAATGGTATCACAG
ACCCTTTGATTCAAGCAGATTATTATGAACCAATGGCATGCGGGAAAGGGGGCTATCACC
CTGTTCTCTCATCAGAAGAATGTGAGAAAATGAGTAAAGCTGCAGGTCGTTGTCGTAGGT
TGAACAAGTTATGTTATGCTTCTAAATCAAGTTTACCATGCATAGTCGCCACTGCTTACT
GTGACTCTGCACTTTTGGAACCGTACATTAACACAGGACTCAACGTCTATGACATTAGAG
GGCCCTGTGAAGATAATAGTACTGATGGTATGTGTTATACAGGTCTCCGCTATGTCGACC
AGTATATGAATTTTCCTGAAGTTCAAGAAACGCTAGGGTCCGACGTGCATAATTATTCTG
GCTGTGATAATGACGTGTTCACCGGATTTTTGTTTACGGGCGATGGAAGTAAACCATTTC
AACAATATATTGCTGAATTATTAAATCACAACATTCCGGTATTAATATATGCGGGTGATA
AGGATTATATTTGTAATTGGCTGGGAAACCATGCTTGGTCCAATGAGTTGGAATGGATCA
ATAAACGTAGGTATCAGAGAAGGATGTTAAGACCATGGGTCAGTAAAGAAACAGGTGAAG
AGTTGGGACAAGTCAAGAACTATGGCCCTTTCACCTTTTTGAGAATATACGATGCCGGTC
ATATGGTGCCCTATGATCAACCGGAGGCAAGTTTGGAAATGGTCAACAGTTGGATTTCCG

GTAATCGTGCTTTTTCGGATCTTTCCACCTTGGAAAATGCTAGTTAG

>YBR139W, 508 aa (SEQ ID NO 56)
MKYLNLVFVLQLLISIKYASFGRAFSLFEDDTTFANLDKQLKLPQNTQQTLKLDRLNHDD
PLFTTFISSVDTDYSLRLRTVDPSKLGIDTVKQWSGYMDYKDSKHFFYWFPESRNDPAND
PIILWLNGGPGCSSFTGLLFELGPSSIGADMKPIHNPYSWNNNASMIFLEQPLGVGFSYG
DEKVSSTKLAGKDAYIFLELFFEAFPHLRSNDFHIAGESYAGHYIPQIAHEIVVKNPERT
FNLTSVMIGNGITDPLIQADYYEPMACGKGGYHPVLSSEECEKMSKAAGRCRRLNKLCYA
SKSSLPCIVATAYCDSALLEPYINTGLNVYDIRGPCEDNSTDGMCYTGLRYVDQYMNFPE
VQETLGSDVHNYSGCDNDVFTGFLFTGDGSKPFQQYIAELLNHNIPVLIYAGDKDYICNW
LGNHAWSNELEWINKRRYQRRMLRPWVSKETGEELGQVKNYGPFTFLRIYDAGHMVPYDQ
PEASLEMVNSWISGNRAFSDLSTLENAS

>YCL052C, 1751 bp, CDS: 501-1751 (SEQ ID NO 67)
TGCACATGTTGAGTATGCGTATTGGGCATTTTCCTATTCTGAGAAGGAGTATGAAATAAT
TGCCGAGGGTTCAGAATGCTCTTTTAGAAATAAAAATGAATGTAAATAGTTGGAATGTAT
CTTTAAGTAGACAAATGCAGGTAAGTTTTAGTGGCCTTTGCGGATTAACAGTATGCTCTT
AGTGCAAAACACGAAAAGAGCTCCCAATCTTTGAACACAATCGACCACGGAGGAACAATA
CACGTAGAAGGGGATAACTAAAACTTTGTCGTGCAAGAGTATTGGAGGACACACTAACAG
CAGAACTTTGCCTTCTTAACTCTTGTTTATGATTGCTTGAAGTATTACACATGTAATAAA
AGATGATTATTTTTTTTTTCCTAAAAAAAGTTCCTTTCTTTGAAGATCCCCCTGATAAAA
AAGATCAAATAATGGAAACGCTAATCATAATCAAATCGGGAGGAGAATAAACGCAAGAAG
TGTGCGTTTCTAGCTGAGTAATGGTGACAAGACATAGAGTGACTGTACTCTACAATGCCC
CTGAGGATATCGGTAATCATATGCGCCAAAATGACACTCATTTGACTGTTCGTGGAGGTT
CTGGTGTGGTTTTACAACAAAGGTGGCTATTAGAGAGGACTGGAAGCTTGGATAAATCCT
TTACGAGAATCACTTGGAGGCCCAGAGCGGACTTGGCTAGAAGTTTAAGCGTTATAGAAA
ATGAACTGAGTGCTGGCTTTTCAGTTTACTCAAATTCTTCGGATGTGCCGGAAAGGTTTA
TTACTAACCCAGTCTACAATTCATTTCACAGTGAGAAGTTTGACATAGAGCAGTACTTGC
CTCCCGAAGTAGATTTGAATCTGTCATGGAATCCAGAAGATTTTACATATGATATATCAG
TGGAGCCCACACAAATCCAAATTGTTGAATATCGTCTGTTGAAACAGGGTGAAGAATTTA
CAATTGCAAGAGTGAAAGATGAGAAACTCGAAGTAGGTGTATTCTTTGTGGATGCAAGTG
ATGAAAGTGATGTCGATATTGGTGGAATACGTTGTAATTGGAGGATGGACGATGGTAAAA
TGGAAAGATGTCAGAAAACATCCTTATTGTATAAACAGGGCCATATCGCATACAATCACT
CGACGACTACGACATCACTATATCTGAATGAACCTATCGGTTTGCATCCAAAATCATGA
TTGATCTCACAGATTTCGAAGAACGCCCTAAATGCATGTATCTAATGCACCTGCAATTGC
CGTTAGAATTATTTATCGATAAATTCCAATCCTCTCCCTTACTACTTTTGGAGAAGACG
ACTTAGAATTACCAGAATACTCTCTTCGAGATAAGGCATGGGGTTCTGAAAGTATCTTTG
AATTGAAAGCCGGCACAATGAATGAAGTGACATTGCATACTAGATATATTGAGCCTTCTA
ATAATAAAGGGGATAAATTAGAAGTTTCATTTGATCCAGAAGTTATATTAGCCTGCGACA
CAGGTGACAATAAAGTTTCCCGTAATCCATTTTATAAAAAAGGTCTAGGATATGAATCTC
TCTTTACAGACGATACTACATTCCGCCATTTGAACTCGACAACTCTTCTAGTACCAATTC
CAAGGCCTGACACAAAGGATTATTCCAAGATCAAAAATGGTACGTTACTATGCTTACTCA
TCTCCATCATATACATTTTCTCCAAGGTATTTGGTAACAACAAGAAGAAAAGATCAGTAA
AACGGGAATAA

>YCL052C, 416 aa (SEQ ID NO 68)
MVTRHRVTVLYNAPEDIGNHMRQNDTHLTVRGGSGVVLQQRWLLERTGSLDKSFTRITWR
PRADLARSLSVIENELSAGFSVYSNSSDVPERFITNPVYNSFHSEKFDIEQYLPPEVDLN
LSWNPEDFTYDISVEPTQIQIVEYRLLKQGEEFTIARVKDEKLEVGVFFVDASDESDVDI
GGIRCNWRMDDGKMERCQKTSLLYKQGHIAYNHSTTTTSLYLNEPIGLHPKIMIDLTDFE
ERPKCMYLMHLQLPLELFIDKFQSSPLLLFGEDDLELPEYSLRDKAWGSESIFELKAGTM
NEVTLHTRYIEPSNNKGDKLEVSFDPEVILACDTGDNKVSRNPFYKKGLGYESLFTDDTT
FRHLNSTTLLVPIPRPDTKDYSKIKNGTLLCLLISIIYIFSKVFGNNKKRSVKRE

>YCR009C, 1298 bp, CDS: 501-1298 (SEQ ID NO 73)
GTACAAAAATGATTACGAAAATATAGATGATGTAAGCAAGGTACGGTTATAAACAGTTAA

CATATAAGTTTACTTCACTTTTTTGCTGACTCCTTTACTTGTCTTCCCTGCACTTTGATT
TTACTTCAGAAAAAATAAGATATATGTTTCTGATAAAACTTTTAGGTTAGCGGAGAAGAT
GTTGCCACGAATATCATGTAATTGAAAGGCAACGAAAGGTCTATCGTTTGCCATTCATAA
TGTGATTCGACTTGTCTTTTTCATTGTAACAGACATGAAACGTTTCCTTTACGTCCCTAT
GAATTTTTGTTGGCTGAACTGGGCGCTGCAGGGGCTGGACGATCCAAATGCGCGGATTTT
GAACAATTATGAGAATCCGAATTAAAAGAAAGGGAAAACAAATTTAATAACAGGCAGACG
TGAGAGAAGAAAGGAAACGCTGTGATATAGAAAACTATACAAATCCTATTATAAGAAGC
CAGAAGAAAGCTGATACAAGATGAGTTGGGAAGGTTTTAAGAAAGCTATCAACAGAGCTG
GTCACAGTGTGATAATTAAGAATGTCGACAAGACCATTGATAAAGAGTATGACATGGAAG
AACGTCGTTATAAAGTTCTTCAAAGAGCAGGTGAGGCATTACAAAAGGAAGCCAAAGGTT
TCTTGGACTCATTGAGAGCTGTGACAGCATCACAGACTACCATTGCCGAGGTCATCTCTA
ACCTCTATGACGATTCAAAATATGTTGCTGGTGGTGGTTACAACGTTGGTAACTATTATT
TGCAATGTGTTCAAGATTTTGATAGCGAAACTGTTAAGCAATTAGACGGGCCCTTAAGAG
AAACCGTACTAGATCCAATAACAAAGTTTTCGACGTATTTCAAAGAAATTGAGGAGGCCA
TAAAAAAGAGAGACCATAAGAAACAAGACTTCGATGCTGCGAAGGCAAAAGTTCGTAGAT
TAGTGGACAAACCTGCTAAAGATGCCTCTAAACTGCCAAGGGCTGAAAAAGAATTGAGCT
TAGCTAAAGATATTTTCGAAAATCTTAATAACCAATTGAAAACTGAACTACCACAGTTAG
TTTCATTAAGAGTACCTTACTTTGACCCAAGTTTTGAAGCTTTAATCAAGATTCAGCTAA
GGTTCTGTACTGATGGTTACACTCGTTTAGCGCAGATTCAACAATATTTGGACCAACAAT
CAAGAGACGACTATGCCAATGGGTTATTAGACACTAAAATCGAAGAACTATTAGGACAAA
TGACAAGCCTAGATATTTGTGCGCTCGGGATAAAATAA

>YCR009C, 265 aa (SEQ ID NO 74)
MSWEGFKKAINRAGHSVIIKNVDKTIDKEYDMEERRYKVLQRAGEALQKEAKGFLDSLRA
VTASQTTIAEVISNLYDDSKYVAGGGYNVGNYYLQCVQDFDSETVKQLDGPLRETVLDPI
TKFSTYFKEIEEAIKKRDHKKQDFDAAKAKVRRLVDKPAKDASKLPRAEKELSLAKDIFE
NLNNQLKTELPQLVSLRVPYFDPSFEALIKIQLRFCTDGYTRLAQIQQYLDQQSRDDYAN
GLLDTKIEELLGQMTSLDICALGIK

>YCR010C, 1352 bp, CDS: 501-1352 (SEQ ID NO 75)
GAGCTCCGTGGAATAGGCGAGCGGCTGAGTGGTTCTCCAAGCTACGGTTTTTTACGTCTAG
CCCCATGTGAGCAAGCCAAACAAGGGCCCTTAAAGGCGTGACTACAAAAAGGGGCGGGTT
GGAAGGTCATCTGCAGCGAGATACGAAAAGATTTTTTGCCAGATTTGCGGTTGGGCGGCT
ATTTCGGTATTGTTGGGGTAACAAACGTTGGGGAAGACTGCATTTTCTTACAGCTTTTTT
TCGTTATCGCGGGTTGGGCGGCTATGGCGCCTTCTCCTCTGTACTCCAACCTGTCAGAGA
CACCAAGCTGTATATAAAGCACCTTGGTTGGATCGTATTTCCCTGAGATCTTGCTATAGG
TTCATTTTATATATCGTCCAATAGCAATAACAATACAACAGAAACTACTAGCATCTGTTT
ATAAGAAAAAGGCAAATAGTCGACAGCTAACACAGATATAACTAAACAACCACAAAACAA
CTCATATACAAACAAATAATATGTCTGACAAGGAACAAACGAGCGGAAACACAGATTTGG
AGAATGCACCAGCAGGATACTATAGTTCCCATGATAACGACGTTAATGGCGTTGCAGAAG
ATGAACGTCCATCTCATGATTCGTTGGGCAAGATTTACACTGGAGGTGATAACAATGAAT
ATATCTATATTGGGCGTCAAAAGTTTTTGAAGAGCGACTTATACCAAGCCTTTGGTGGTA
CCTTGAATCCAGGGTTAGCTCCTGCTCCAGTGCACAAATTTGCTAATCCTGCGCCCTTAG
GTCTTTCAGCCTTCGCGTTGACGACATTTGTGCTGTCCATGTTCAATGCGAGAGCGCAAG
GGATCACTGTTCCTAATGTTGTCGTCGGTTGTGCTATGTTTTATGGTGGTTTGGTGCAAT
TGATTGCTGGTATTTGGGAGATAGCTTTGGAAAATACTTTTGGTGGTACCGCATTATGTT
CTTACGGTGGGTTTTGGTTGAGTTTCGCTGCAATTTACATTCCTTGGTTTGGTATCTTGG
AAGCTTACGAAGACAATGAATCTGATTTGAATAATGCTTTAGGATTTTATTTGTTGGGGT
GGGCCATCTTTACGTTTGGTTTAACCGTTTGTACCATGAAATCCACTGTTATGTTCTTTT
TGTTGTTCTTCTTACTAGCATTAACTTTCCTACTGTTGTCTATTGGTCACTTTGCTAATA
GACTTGGTGTCACAAGAGCTGGTGGTGTCCTGGGAGTTGTTGTTGCTTTCATTGCTTGGT
ACAACGCATATGCAGGTGTTGCTACAAAGCAGAATTCATATGTACTGGCTCGTCCATTCC
CATTACCATCTACTGAAAGGGTAATCTTTTAA

>YCR010C, 283 aa (SEQ ID NO 76)
MSDKEQTSGNTDLENAPAGYYSSHDNDVNGVAEDERPSHDSLGKIYTGGDNNEYIYIGRQ

KFLKSDLYQAFGGTLNPGLAPAPVHKFANPAPLGLSAFALTTFVLSMFNARAQGITVPNV
VVGCAMFYGGLVQLIAGIWEIALENTFGGTALCSYGGFWLSFAAIYIPWFGILEAYEDNE
SDLNNALGFYLLGWAIFTFGLTVCTMKSTVMFFLLFFLLALTFLLLSIGHFANRLGVTRA
GGVLGVVVAFIAWYNAYAGVATKQNSYVLARPFPLPSTERVIF

>YCR021C, 1499 bp, CDS: 501-1499 (SEQ ID NO 79)
ATCGAAAGCGTGCTTTGTAAGAATATTTGGTATGGCTAAAGTAAGCAAAGCCATATCCCG
ATCCCGATCCCGACTCTTATTCCGATCCCTTCCGCCACATCCTGCATGTTTATTCGAATA
CCAAATTAGCTCATCTTCGTTATTTCATCATCCCTTTCTGCTATGGCAAGGACAAGTTTT
TTTCTAGCATCTCATCGAAAACTTTCCTCTCCCTAATTGGCCAAAGTTTTCATATTCATC
ATCAGTTAGAAAGTATAATATCAATCCCTTACCTCATTACAAGTTGTATCACACTAAAAA
AATCATATATAAGTCTGTGAGAGTCTTCAATTATTTAGCGTAACACCTATTCACTTTCTA
ATCTTGTTTCTTGTTTTTACATTCTGCAATACAACACAACAACAAATATTAACTCAATTA
TTATTATTTATAATTACAAAAACAAAACAACAAGTTTGAGACTTTAATATCTTTTGATTA
CTAAAAACAACAAATTTCAAATGAACGATACGCTATCAAGCTTTTAAATCGTAACGAGG
CTTTAGGGCTTAATCCACCACATGGCCTGGATATGCACATTACCAAGAGAGGTTCGGATT
GGTTATGGGCAGTGTTTGCAGTCTTTGGCTTTATATTGCTATGCTATGTTGTGATGTTCT
TCATTGCGGAGAACAAGGGCTCCAGATTGACTAGATATGCCTTAGCTCCTGCATTTTTGA
TCACTTTCTTTGAATTTTTTGCTTTCTTCACTTATGCTTCTGATTTAGGTTGGACTGGTG
TTCAAGCTGAATTTAACCACGTCAAGGTTAGCAAGTCTATCACAGGTGAAGTTCCCGGTA
TTAGACAAATCTTTTACTCGAAATATATTGCCTGGTTCTTGTCCTGGCCATGCCTTTTAT
TTTTAATCGAGTTAGCCGCTAGTACTACTGGTGAGAATGACGACATTTCCGCCTTGGATA
TGGTACATTCGCTGTTAATTCAAATCGTGGGTACCTTATTCTGGGTTGTTTCGCTATTAG
TTGGTTCATTGATCAAGTCCACCTACAAGTGGGGTTATTACACCATTGGTGCTGTCGCTA
TGTTGGTTACCCAAGGTGTGATATGCCAACGTCAATTCTTCAATTTGAAAACTAGAGGGT
TCAATGCACTTATGCTGTGTACCTGCATGGTAATCGTTTGGTTGTACTTTATCTGTTGGG
GTCTAAGTGATGGTGGTAACCGTATTCAACCAGACGGTGAGGCTATCTTTTATGGTGTTT
TGGATTTATGTGTATTTGCCATTTATCCATGTTACTTGCTAATTGCAGTCAGCCGTGATG
GCAAATTGCCAAGGCTATCTTTGACAGGAGGATTCTCTCATCACCATGCTACGGACGATG
TGGAAGATGCGGCTCCTGAAACAAAAGAAGCTGTTCCAGAGAGCCCAAGAGCATCTGGAG
AGACTGCAATCCACGAACCCGAACCTGAAGCAGAGCAAGCTGTCGAAGATACTGCTTAG

>YCR021C, 332 aa (SEQ ID NO 80)
MNDTLSSFLNRNEALGLNPPHGLDMHITKRGSDWLWAVFAVFGFILLCYVVMFFIAENKG
SRLTRYALAPAFLITFFEFFAFFTYASDLGWTGVQAEFNHVKVSKSITGEVPGIRQIFYS
KYIAWFLSWPCLLFLIELAASTTGENDDISALDMVHSLLIQIVGTLFWVVSLLVGSLIKS
TYKWGYYTIGAVAMLVTQGVICQRQFFNLKTRGFNALMLCTCMVIVWLYFICWGLSDGGN
RIQPDGEAIFYGVLDLCVPAIYPCYLLIAVSRDGKLPRLSLTGGFSHHHATDDVEDAAPE
TKEAVPESPRASGETAIHEPEPEAEQAVEDTA

>YDR073W, 1010 bp, CDS: 501-1010 (SEQ ID NO 91)
GTTAGCTTGCCTTGCATTTCCCCATGCGTCTCGAATAGGAATTATTCAAGATGGATTATT
GGCATTACGAGTAACCAAGGATAACCCCGCTGTGCGTGAAACCACCTCTCTTTCACGTT
TCTTCAAGGCCAGTGCAAACGCGAATAAACATATCTACGCTATATATAGATATGACGTTT
CTCAAGCCAACAGAAGTAGATAAAGCAGCCAGGAGGGTAGAGAGTGTTCAAATTATAGCA
AGCCTTCTTCTACCTGTTTTTTTTTTGATGATTGTTTTGCCGGGTAACAATCGACTTTCGG
GCAAATTTTTTTTCCTTTTTTCTCCTAACAGTATATACGGAGTGGAGAACAGACTTCCCA
TAAAAGCATTATTACGTGGGGTCGTAGTAAGATTGCCGTTTATGATACCCTCTATTCAGGG
CTCAGAGCGCATCACGATCGGGAGTGTAAATTCAATGTGCATATAAGCAAAACACACAGA
TTTCCTTTTTTCCCAGAAAAATGAGCAGTGAAATTGCCTACTCGAATACGAACACCAACA
CTGAAAACGAGAACCGCAATACTGGCGCTGGCGTAGATGTAAATACAAATGCAAATGCAA
ATGCAAATGCAACTGCAAATGCAACTGCAAATGCAACTGCAAATGCAACTGCAGAGCTGA
ACCTCCCCACGGTCGATGAGCAAAGACAGTATAAGGTACAACTGCTATTGCATATCAACA
GCATATTACTTGCTAGAGTTATTCAGATGAATAATAGTTTACAAAACAATCTACAGAACA
ATATAAATAATAGCAATAACAATAACATCATCAGGATACAGCAACTTATATCTCAGTTCC
TTAAAAGGGTTCATGCCAATCTTCAATGCATATCTCAGATAAACCAAGGAGTGCCCTCAG

CGAAACCACTGATCCTCACGCCTCCTCAGCTAGCCAACCAGCAGCAACCTCCACAGGATA
TTCTTTCTAAACTCTATCTTCTCTTGGCAAGAGTGTTCGAGATATGGTAG

>YDR073W, 169 aa (SEQ ID NO 92)
MSSEIAYSNTNTNTENENRNTGAGVDVNTNANANANATANATANATANATAELNLPTVDE
QRQYKVQLLLHINSILLARVIQMNNSLQNNLQNNINNSNNNNIIRIQQLISQFLKRVHAN
LQCISQINQGVPSAKPLILTPPQLANQQQPPQDILSKLYLLLARVFEIW

>YDR178W, 1046 bp, CDS: 501-1046 (SEQ ID NO 105)
ACGATTAGGCGTCAAGTCCTTAGACCCCAATGACAACAACACAGCCAACCGTATCATCGA
GGAATTGTTGAAGTGAATAGATAAAAAAAAAACGCACCAAGTAAGTAAGTAAATAAAGAA
TAAATAAACTATATGAGTAAAACACCAAGCGAGGATGTTTCATTGTGCATCCGTGTTCTT
GATGATCACATAACTGTAAAAGAATAATACGGCACGTTAAATGTTATTTTAGAATATATA
AACACCTTATGTGCCATAAGCATTGAGCCAATCGCTGCTGTTTTTTTTATTCCGGGGCAC
CTTCGGAAGAACACAGGCGCAATTTAGTTATATAAGGAGAAGCCCTCGAGCGATCAGGGG
ACCGACTGCGGATCGCTTAAGGCAAAGATAGAAGGATAAATATCTGCTTTGGAAGATAG
TCGTATCTAATTTCCCATTCTGTTGTTTTCTTGATCTTTCCTACGCTTTCGACTTTCTTC
CTACGCGCTTTATAATAGCTATGATGTTGCCAAGATCCATGAAATTTATGACTGGAAGGA
GAATTTTCCATACTGCCACAGTAAGGGCCTTCCAGTCTACCGCTAAGAAGAGCTTAACTA
TCCCATTTTTGCCCGTATTACCCCAGAAACCAGGTGGTGTTAGGGGCACTCCCAATGATG
CCTACGTCCCCCCCCCCTGAGAATAAATTAGAGGGCTCATACCACTGGTATATGGAAAAAA
TCTTTGCCTTGTCCGTCGTTCCATTGGCTACGACGGCTATGCTGACAACCGGTCCGTTAT
CCACTGCAGCTGATTCTTTCTTTTCTGTCATGCTTTTGGGATATTGTTACATGGAATTTA
ACTCTTGTATCACCGATTATATTTCTGAAAGAGTTTATGGTGTTTGGCACAAGTACGCCA
TGTATATGTTGGGCCTTGGTTCTGCGGTCTCCCTTTTTGGAATCTATAAACTAGAAACCG
AGAATGATGGTGTTGTTGGTTTAGTAAAAAGTCTATGGGATTCTTCCGAGAAAGACAACA
GTCAAAAGATTGAAGCCAAGAAGTAG

>YDR178W, 181 aa (SEQ ID NO 106)
MMLPRSMKFMTGRRIFHTATVRAFQSTAKKSLTIPFLPVLPQKPGGVRGTPNDAYVPPPE
NKLEGSYHWYMEKIFALSVVPLATTAMLTTGPLSTAADSFFSVMLLGYCYMEFNSCITDY
ISERVYGVWHKYAMYMLGLGSAVSLFGIYKLETENDGVVGLVKSLWDSSEKDNSQKIEAK
K

>YDR202C, 1556 bp, CDS: 501-1556 (SEQ ID NO 107)
GAATTCCAACCGGAAATTGCAAACAGCAGCAATTTCTCGTACCGATGAAGGGGAACATGG
CCGTTGTACCGAGGTTCCATTGGCCGAGTATTAGCCAGGGCCCTAATACGTAACTCGGTA
CGCTCTTCAGCTTCTTTCGCATAATCAACGTTCTTGTTATGTAACTCACCACGTTCCATG
GCATCCGCCAACCTTGCTTCCTTACCAAATATTAATGAGCCTAAGGTGTACATTGCCGCC
GCAGGTAATATTAGCCCACGACGTTGGCATTTCACTGGCAAAGTAGCTGTTGATCTCAGT
AAAGATAACCTCAACATACTCTTTTACTTGTCCTTTTTGTAGCTAATTGCTTTCCTCCC
CTTCTTTTCCACAAACCGCAACTATTTTTCTCTCAAAAGTTATATGAAGTATATATACTG
AATGGAGCAATTCGGGGTTGAGTGAATTACAAAATTATAGTATCTGATCAAGCACACAGT
GGAAGTGCTCGAAAAGCAATATGAGTGTTGATTTGTTTCCAAATGATAGATTTGGTGCAG
AAGATAAATACGACAACTTTAAGGATGCCGTAAAAGAATGCTCCTGGCTCATCGAAGAAA
TCGTCAAACCGCAATTACCCAACATTATTGACAACTTTTCTAAATGCCTAGAGATGCTAG
AGAGTGACCAAATATTCAAAATGCCTGTATCTAATGGTATTCCCACGAAAGTAACAAAC
AAAACGACTCTCCGACGGTAAAGGGTGTTATCACAAGACAAGGCCAATACATTGTTGACT
TTCACATTGTTGTCAGATTCCCACAATTTCAAAGGGGTAAACAAGTTATGTTCCGAATGA
ATACGGGACTGAATTTCTTACTTATTCAATTCAGTAAGATAATGACGCACTTGAAAAATA
TTTTGGAAATACTGAATCAACTTCAAGTAGCTACAGATGTCAGCGAATTCGTATCCAAAT
TTGGCGTGGCCATGGAACTTTTGAACCATTCTCTAATACTTTTACAAAATCCTCCTAGAG
ACCTGGTATTCCCAGAAGATAACAACTTTGCTATGAAGGAAATGTTCCAGGATTGTTACT
CAGTCTGCGAATCCACAGCTCACATCCTAGGACTGGAACTTACGCTTTGTAGGAATGAGC
TTTGCATAGAACTACGAAATCTAATTAAGGTGACTAAAAAACCTTGGTGCGAGATTGATA
GTAAAACTGGCAGGTCATTTTGCGACCAAATAAGAAATCAAGTGACAAATGAAAGAAACA

AAACTTTATCTAAGATCCTCTCAGAAAACGGTGTACAAGTCCAGGATTCCACATTACTTA
ACCACATAATTTCTTCTTTTCAAAGTGAAGCTATAACACTTCCAGAAGCTCAGGAATTAT
TAAGAAGGGGCGTTACTTTCGATAATAGGGTAGTCATGGAATGTGAAAAGTTAATAGTAT
CTACAAGTGATCCAACTTTGATCAGTATAAGCGCCAAATTGAACAGTCTCAAAGCTTCGA
TGGCGAACCATCAAGCAAATTTGGTAGCTAGCAAACAGTTAAGTACATATAAGTAA

>YDR202C, 351 aa (SEQ ID NO 108)
MSVDLFPNDRFGAEDKYDNFKDAVKECSWLIEEIVKPQLPNIIDNFSKCLEMLESDQIFK
MPVSNGIPNESNKQNDSPTVKGVITRQGQYIVDFHIVVRFPQFQRGKQVMFRMNTGLNFL
LIQFSKIMTHLKNILEILNQLQVATDVSEFVSKFGVAMELLNHSLILLQNPPRDLVFPED
NNFAMKEMFQDCYSVCESTAHILGLELTLCRNELCIELRNLIKVTKKPWCEIDSKTGRSF
CDQIRNQVTNERNKTLSKILSENGVQVQDSTLLNHIISSFQSEAITLPEAQELLRRGVTF
DNRVVMECEKLIVSTSDPTLISISAKLNSLKASMANHQANLVASKQLSTYK

>YDR256C, 2048 bp, CDS: 501-2048 (SEQ ID NO 115)
GGGAAGAACTAAGAGATGTTATGGCTCGGAGAGTTTTGAAAAGCGAAATAGATTCGCTGC
AAGTTTGTGAAGAAACCATCGACAAGAATTACAAGGTTATTCCTGATGAAAAGCTGCTAA
CTAATATTTTAAAGAGAAAGTTGACAGAGGAAGAAAAAAGCTCTGTCAAACGTCCTTGCG
TGAAGAAGTGAGCGGTTGTTCTAACCACTATTTAAAGCCGCAATTAGTAATGCAAAAAGT
TGGCCGGAATTAGCCGCGCAAGTTGGTGGGGTCCCTTAATCCGAAAAAGGACGGCTTTAA
CAAATATAAACTCCGAAAATCCCCACAGTGACAGAATTGGAGAAACAACCAGTTTTGATA
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TTGAATTTCTTGTAGGTTTATTTAAAAGGTAAGTTAAATAAATATAATAGTACTTACAAA
TAAATTTGGAACCCTAGAAGATGTCGAAATTGGGACAAGAAAAAAATGAAGTAAATTACT
CTGATGTAAGAGAGGATAGAGTTGTGACAAACTCCACTGGTAATCCAATCAATGAACCAT
TTGTCACCCAACGTATTGGGGAACATGGCCCTTTGCTTTTGCAAGATATAACTTAATTG
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CTGGTGCCTTCGGCTATTTTGAAGTAACCGATGACATTACTGATATCTGCGGGTCTGCTA
TGTTTAGTAAAATTGGGAAAAGAACGAAATGTCTAACAAGATTTTCGACTGTGGGTGGTG
ATAAAGGTAGTGCCGACACGGTTCGTGATCCAAGGGGGTTTGCCACCAAATTCTACACTG
AAGAAGGTAATTTAGATTGGGTCTACAATAATACACCGGTATTCTTTATCAGAGACCCTT
CCAAGTTCCCTCACTTTATCCACACACAGAAGAGAAACCCACAAACCAACCTAAGGGATG
CTGACATGTTTTGGGATTTCCTCACCACTCCTGAAAATCAGGTGGCCATTCATCAAGTAA
TGATCCTTTTTTCAGACCGTGGTACCCCTGCCAACTACCGTAGTATGCATGGTTATTCTG
GTCATACCTATAAATGGTCCAATAAAAACGGAGATTGGCATTATGTGCAAGTTCATATCA
AAACCGATCAAGGAATAAAGAATTTGACCATAGAAGAGGCTACCAAAATTGCGGGATCCA
ATCCAGATTACTGCCAGCAGGATTTATTTGAGGCTATTCAGAATGGAAACTATCCTTCCT
GGACAGTTTATATTCAAACAATGACCGAACGCGATGCCAAAAAATTACCATTTCTAGTCT
TTGATTTGACTAAAGTATGGCCTCAGGGGCAATTCCCTTTACGGCGTGTGGGTAAGATTG
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GTACCACGGTTCCTTACCAAGAAGCAAGCGCTGATCCAGTATTACAGGCCCGTTTGTTTT
CATATGCGGATGCTCATAGATACAGGCTAGGTCCTAACTTCCATCAAATACCCGTAAACT
GTCCATATGCATCTAAATTTTTCAATCCCGCTATCAGAGATGGACGTGATAATGTTAACG
GCAACTTCGGCTCAGAACCTACATATTTGGCCAACGATAAATCGTACACGTATATCCAAC
AGGACAGACCCATTCAACAACACCAAGAGGTATGGAATGGGCCAGCTATCCCTTATCATT
GGGCAACATCCCCAGGTGATGTAGATTTCGTGCAAGCAAGAAATCTCTACCGCGTTTTGG
GTAAACAACCTGGACAGCAAAAGAACTTGGCATATAACATCGGCATTCATGTAGAAGGCG
CCTGTCCTCAAATACAGCAGCGGCGTTTATGATATGTTTGCTCGTGTTGATAAGGGACTAT
CTGAGGCAATTAAAAAAGTAGCTGAGGCAAAACATGCTTCTGAGCTTTCGAGTAACTCCA
AATTTTGA

>YDR256C, 515 aa (SEQ ID NO 116)
MSKLGQEKNEVNYSDVREDRVVTNSTGNPINEPFVTQRIGEHGPLLLQDYNLIDSLAHFN
RENIPQRNPHAHGSGAFGYFEVTDDITDICGSAMFSKIGKRTKCLTRFSTVGGDKGSADT
VRDPRGFATKFYTEEGNLDWVYNNTPVFFIRDPSKFPHFIHTQKRNPQTNLRDADMFWDF
LTTPENQVAIHQVMILFSDRGTPANYRSMHGYSGHTYKWSNKNGDWHYVQVHIKTDQGIK

NLTIEEATKIAGSNPDYCQQDLFEAIQNGNYPSWTVYIQTMTERDAKKLPFSVFDLTKVW
PQGQFPLRRVGKIVLNENPLNFFAQVEQAAFAPSTTVPYQEASADPVLQARLFSYADAHR
YRLGPNFHQIPVNCPYASKFFNPAIRDGPMNVNGNFGSEPTYLANDKSYTYIQQDRPIQQ
HQEVWNGPAIPYHWATSPGDVDFVQARNLYRVLGKQPGQQKNLAYNIGIHVEGACPQIQQ
RVYDMFARVDKGLSEAIKKVAEAKHASELSSNSKF

>YER103W, 2429 bp, CDS: 501-2429 (SEQ ID NO 145)
ACTATTGTCACTTCTCCATTGAGATTCGAAAAACCCCTCGGGTCTTGTTAGAACTAAATT
ACGTTCATAGGGGTGGGATTTATATTGTAATTCCGCGAGGTTTACACGAAAGATATCTCA
ACTCTAGCCGCACATCCATTCCGGTATGTACTCTCCCACCATTGGGTATTATAGAATGTA
ATAGGTTTCAAAGCGGATATCTTTTGCCCGGTGAGTTGTTACTTTTCATTCGAGCAATG
AAGTACATTCTAGAAGTTCCTAGAACCTTATGGAAGCACCAAGAAAAAAGGAAGTTAAAC
AAAACACTGATTCAATAAGCAAGGGGGAAGCTCCTTAGTTTGACGACAGTAACAAAATG
TTCGTATAAATTGAACGAAACTCAAGCCAATAAAGGACTTTTCAGAGGCCTATCTCTTCT
TTCTCCACAACTTTCGAATAAAAACCACTAATAAAAAGTAAATAACAAAAACAAGAAAAA
AAATAAACAAAACAATAATCATGTCAAAAGCTGTTGGTATTGATTTAGGTACAACCTATT
CATGTGTTGCTCATTTTGCAAACGATAGGGTTGAAATTATCGCTAACGATCAAGGTAATA
GAACGACGCCTTCTTATGTGGCTTTTACTGACACAGAAAGGCTAATTGGTGACGCTGCGA
AGAATCAAGCTGCGATGAACCCACATAATACAGTATTCGATGCTAAGCGTCTGATCGGAC
GTAAATTCGATGATCCAGAAGTGACGAACGATGCTAAGCATTACCCATTCAAAGTGATTG
ACAAGGGAGGTAAACCGGTAGTGCAAGTGGAATATAAAGGCGAGACAAAGACATTTACTC
CAGAAGAAATTTCCTCAATGATCTTGACAAAGATGAAGGAGACTGCTGAGAACTTTTTAG
GAACAGAAGTGAAAGATGCTGTAGTAACGGTTCCAGCCTATTTCAACGATTCACAAAGGC
AAGCAACAAAAGATGCCGGTACAATCGCGGGCTTGAACGTTCTTCGTATCATTAATGAAC
CTACAGCTGCCGCTATTGCGTATGGGCTGGACAAGAAATCGCAGAAGGAGCACAACGTCT
TGATCTTTGATTTAGGTGGTGGTACTTTTGATGTCTCTCTGCTATCCATAGATGAAGGTG
TCTTTGAGGTTAAGGCTACTGCTGGTGACACTCACTTGGGTGGTGAAGATTTCGATAGTA
GGCTGGTTAACTTTCTAGCCGAGGAGTTCAAAAGAAAAAATAAAAAGGATCTAACAACTA
ACCAAAGGTCCCTAAGGAGGTTAAGGACCGCCGCTGAAAGGGCCAAGAGAACTCTGTCTT
CGTCTGCTCAGACATCTATAGAAATAGATTCATTATTTGAGGGTATCGATTTCTATACTT
CCATTACAAGGGCAAGATTTGAAGAATTATGTGCTGATTTGTTTAGATCTACATTGGAGC
CAGTGGAAAAAGTTTTGGCTGATTCAAAATTAGATAAGTCACAAATTGATGAAATTGTAC
TTGTTGGTGGTTCAACAAGAATTCCAAAAGTACAAAAACTGGTTTCTGATTTTTTCAATG
GTAAAGAACCAAACCGTTCGATTAACCCTGATGAGGCCGTCGCTTATGGTGCTGCCGTAC
AGGCTGCCATCTTAACGGGTGACCAGTCGTCGACGACCCAAGATTTACTGTTGCTGGATG
TTGCACCATTATCTCTAGGTATTGAAACTGCAGGTGGTATTATGACAAAGTTGATCCCAA
GAAATTCGACTATCCCAACAAAAAAATCGGAAGTGTTTTCCACCTACGCTGACAACCAAC
CTGGTGTGTTGATACAAGTTTTGAGGGTGAAAGGACAAGGACAAAAGACAACAATCTAC
TGGGTAAATTTGAGTTGAGCGGTATTCCACCCGCTCCAAGAGGCGTACCACAAATTGAAG
TTACATTTGATATCGATGCAAATGGTATTCTGACCGTATCTGCCGTTGAAAAAGGTACTG
GTAAATCTAACAAGATTACAATTACTAACGATAAGGGAAGATTATCGAAGGAAGATATCG
ATAAAATGGTTGCTGAGGCAGAAAAGTTCAAGGCCGAAGATGAACAAGAAGCTCAACGTG
TTCAAGCTAAGAATCAGCTAGAATCGTACGCGTTTACTTTGAAAAATTCTGTGAGCGAAA
ATAACTTCAAGGAGAAGGTGGGTGAAGAGGATGCCAGGAAATTGGAAGCCGCCGCCCAAG
ATGCTATAAATTGGTTAGATGCTTCGCAAGCGGCCTCCACCGAGGAATACAAGGAAAGGC
AAAAGGAACTAGAAGGTGTTGCAAACCCCATTATGAGTAAATTTTACGGAGCTGCAGGTG
GTGCCCCAGGAGCAGGCCCAGTTCCGGGTGCTGGAGCAGGCCCCACTGGAGCACCAGACA
ACGGCCCAACGGTTGAAGAGGTTGATTAG

>YER103W, 642 aa (SEQ ID NO 146)
MSKAVGIDLGTTYSCVAHFANDRVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQAAMN
PHNTVFDAKRLIGRKFDDPEVTNDAKHYPFKVIDKGGKPVVQVEYKGETKTFTPEEISSM
ILTKMKETAENFLGTEVKDAVVTVPAYFNDSQRQATKDAGTIAGLNVLRIINEPTAAAIA
YGLDKKSQKEHNVLIFDLGGGTFDVSLLSIDEGVFEVKATAGDTHLGGEDFDSRLVNFLA
EEFKRKNKKDLTTNQRSLRRLRTAAERAKRTLSSSAQTSIEIDSLFEGIDFYTSITRARF
EELCADLFRSTLEPVEKVLADSKLDKSQIDEIVLVGGSTRIPKVQKLVSDFFNGKEPNRS

INPDEAVAYGAAVQAAILTGDQSSTTQDLLLLDVAPLSLGIETAGGIMTKLIPRNSTIPT
KKSEVFSTYADNQPGVLIQVFEGERTRTKDNNLLGKPELSGIPPAPRGVPQIEVTFDIDA
NGILNVSAVEKGTGKSNKITITNDKGRLSKEDIDKMVAEAEKFKAEDEQEAQRVQAKNQL
ESYAFTLKNSVSENNNFKEKVGEEDARKLEAAAQDAINWLDASQAASTEEYKERQKELEGV
ANPIMSKFYGAAGGAPGAGPVPGAGAGPTGAPDNGPTVEEVD

>YER150W, 947 bp, CDS: 501-947 (SEQ ID NO 149)
ATACGGGGGAAGAAGAAATATCATATTCAAAGCTAATTCATTGAAATTAGTGCTTGTCTC
ATCTAGCCTTTAGTGCTTAATCTCTGGAGGAGCACATATGGGGTTAAAGCCATGCCGGGA
CTGGGGGCCCCTATCGGGGCTCGAACCCGAATCCCGCGAGTATTTATTTGAAGGTCCGGG
ACGCAAGTTACCTAATCTGGTTAATTGATATCCCATTTAGGCGATGACGTTCCTTCCCCT
CACCCCTCGGCTTGTTAGAAGATCTATTGTTATAGCCTCCTCTGGAAGAATTTATGCCAG
ATGAAGAAAAAAACTTCTCGAAGTTCCCAGATGCCCAAATGAGGGCTTTCCATCCCTGTT
AGCTGGAAAAGTGTAAGTATATCTATATAAAAAGTCGGCCTACTTTTGCCAGGTTCGTCT
TTCACTTGCACTCTCTTGATCTTACTTTCTACTCAAAAAGAATCCAATACACAAAAATAA
AATCAGTACTATTACTAATAATGTTGTCTAACGCTAAGCTCCTTCTATCATTGGCCATGG
CCTCTACGGCTCTCGGATTGGTATCTAATTCTAGTTCCTCTGTAATCGTGGTACCATCAA
GCGATGCTACTATTGCCGGTAACGATACAGCCACGCCAGCACCAGAGCCATCATCCGCCG
CTCCAATATTCTACAACTCGACTGCTACTGCAACACAGTACGAAGTTGTCAGTGAATTCA
CTACTTACTGCCCAGAACCAACGACTTTCGTAACGAATGGCGCTACATTCACTGTTACTG
CCCCAACTACGTTAACAATTACCAACTGTCCTTGCACTATCCGAGAAGCCTACTTCAGAAA
CATCGGTTTCTTCTACACATGATGTGGAGACAAATTCTAATGCTGCTAACGCAAGAGCAA
TCCCAGGAGCCCTAGGTTTGGCTGGTGCAGTTATGATGCTTTTATGA

>YER150W, 148 aa (SEQ ID NO 150)
MLSNAKLLLSLAMASTALGLVSNSSSSVIVVPSSDATIAGNDTATPAPEPSSAAPIFYNS
TATATQYEVVSEFTTYCPEPTTFVTNGATFTVTAPTTLTITNCPCTIEKPTSETSVSSTH
DVETNSNAANARAIPGALGLAGAVMMLL

>YFR033C, 944 bp, CDS: 501-944 (SEQ ID NO 155)
ATCGAGCCATTCGCGGTCGCTGAGTAAGCGACGGTCATCGGGCGCGCTCGTGGACGATGA
CAAGCGCGAATCACACAAGCATGCAGAGCAAGCACGGCGTAATCGATTAGCGGTCGCGCT
GCACGAACTGGCGTCTTTAATCCCCGCGGAGTGGAAACAGCAAAATGTGTCGGCCGCGCC
GTCCAAAGCGACCACCGTGGAGGCGGCCTGCCGGTACATCCGTCACCTACAGCAGAACGT
GAGCACGTGACCGTGCACCAATGGGAAGCACGTTCCGGGCATATCGGACTGGGCGCGCC
TCCCCTGCGCGGTGCTTGTTATAAGAGGCGCTTTGCTGGAAAGTGGCCCACACCGGGTTT
TCGAGATTAGGACCTACTCAGTCTTAAGGGCAGTATTGGTTGGCGCTTATTTGCACATAT
TGTATACACGCACTCACATTAACAGAAGCACACATATACACTTACACCTACACACACGGA
TAAAGAAAAAGAAATAGAAAATGGGCATGTTGGAACTAGTTGGTGAGTACTGGCAACAAC
TAAAGATAACCGTTGTGCCTGTTGTGGCCGCGGCCGAAGATGACGATAACGAGCAGCATG
AAGAAAAGGCAGCAGAAGGAGAAGAAAAAGAAGAAGAAAATGGGGATGAAGATGAGGATG
AAGACGAAGACGAAGATGATGATGATGACGACGAAGATGAGGAAGAAGAGGAAGAAG
TCACTGATCAGTTGGAAGATTTGAGAGAACATTTCAAGAACACGGAGGAGGGTAAGGCCC
TTGTGCACCACTACGAGGAGTGTGCTGAGAGAGTCAAGATACAGCAACAACAACCCGGCT
ACGCGGATCTTGAACACAAGGAGGACTGTGTGGAGGAGTTTTTCCATCTACAGCACTATT
TGGACACTGCCACGGCACCTAGATTATTTGACAAATTAAAGTAG

>YFR033C, 147 aa (SEQ ID NO 156)
MGMLELVGEYWEQLKITVVPVVAAAEDDDNEQHEEKAAEGEEKEEENGDEDEDEDEDEDD
DDDDEDEEEEEEEVTDQLEDLREHFKNTEEGKALVHHYEECAERVKIQQQQPGYADLEHK
EDCVEEFFHLQHYLDTATAPRLFDKLK

>YGR086C, 1520 bp, CDS: 501-1520 (SEQ ID NO 175)
GTTGAATATTTACCAATTGGGAAAAAGAACTCGTATTTCATTCCCCTTTTTGGAAAGGGG
TGGGGAGAGACTGTTGTTCAGCCACGTCAATTATTATTTTTTCTTTGGCCCTGCGCTTGT
CTTATAAAATTCCGCAGCCGCCTCTTATTTTTTTTTTTTCGATTTTTGGCCCACAGGTC

ATATTGCAAAAACCGAATGGCCGCGCCCCCCTCACGCACGGGACGGAAGAAGGGCGGCGT
CCCCTGTTTTTCTGCTTTGGCTCATCTCTTTGGCTCCGACGGACGAAAGACGGGATTCCC
CCTCCCGTGTCTTTTTATAAATAACAAGTGCTCATTCTGCATCCTTCCTTGTTTCCCGTC
GTTTGGGTACAATGCGTTGATTATCCCAACCCAAGAAAGAAAATTTGTCTCACATCTGCA
TCTGCACATTTATTTACCTATACTTTTCCATTGTTAGCAGTATTGCAAAGTGAAGAATAT
ATCAGCATCAAGTATATAGTATGCACAGAACTTACTCTTTAAGAAATTCCAGGGCACCTA
CCGCCTCTCAATTACAGAACCCACCGCCACCACCATCTACAACCAAAGGTAGATTCTTTG
GGAAGGGTGGTCTAGCTTACAGCTTTAGGAGAAGTGCTGCTGGAGCTTTTGGCCCAGAAT
TATCCAGAAAGTTGTCTCAATTGGTTAAGATTGAAAAGAATGTTTTGAGGTCCATGGAAT
TGACAGCCAACGAAAGACGTGACGCTGCTAAGCAATTGTCTATTTGGGGGTTGGAAAACG
ATGACGATGTTTCCGACATCACTGATAAATTAGGTGTCTTGATCTATGAAGTTAGTGAAT
TAGACGACCAATTTATCGATCGTTATGACCAATACAGATTGACTCTAAAGTCCATCAGAG
ATATCGAAGGTTCTGTTCAACCATCTAGAGACCGTAAGGACAAGATCACCGACAAAATCG
CCTACTTGAAATACAAAGATCCTCAATCACCTAAGATTGAGGTCTTGGAACAAGAATTGG
TGCGTGCTGAGGCTGAATCTTTGGTCGCTGAAGCTCAATTATCTAATATCACAAGGTCAA
AGTTGAGAGCTGCTTTCAACTACCAATTTGACTCCATCATCGAACATTCAGAGAAAATTG
CTTTAATCGCTGGTTACGGTAAGGCTCTCTTGGAACTATTGGACGACTCTCCTGTCACTC
CAGGTGAAACCAGGCCTGCTTACGATGGGTATGAAGCCTCTAAACAAATCATTATTGATG
CTGAAAGCGCACTGAATGAATGGACACTAGACTCTGCCCAAGTCAAGCCTACTTTAAGTT
TCAAGCAGGATTACGAAGACTTCGAACCTGAAGAAGGCGAAGAAGAGGAAGAGGAAGACG
GTCAAGGCAGGTGGTCCGAAGACGAACAAGAAGATGGACAAATTGAAGAACCTGAACAAG
AAGAAGAAGGTGCTGTTGAAGAACATGAACAAGTCGGACACCAGCAAAGTGAGTCTCTTC
CCCAACAAACAACAGCTTAA

>YGR086C, 339 aa (SEQ ID NO 176)
MHRTYSLRNSRAPTASQLQNPPPPPSTTKGRFFGKGGLAYSFRRSAAGAFGPELSRKLSQ
LVKIEKNVLRSMELTANERRDAAKQLSIWGLENDDDVSDITDKLGVLIYEVSELDDQFID
RYDQYRLTLKSIRDIEGSVQPSRDRKDKITDKIAYLKYKDPQSPKIEVLEQELVRAEAES
LVAEAQLSNITRSKLRAAFNYQFDSIIEHSEKIALIAGYGKALLELLDDSPVTPGETRPA
YDGYEASKQIIIDAESALNEWTLDSAQVKPTLSFKQDYEDFEPEEGEEEEEEDGQGRWSE
DEQEDGQIEEPEQEEEGAVEEHEQVGHQQSESLPQQTTA

>YGR197C, 2144 bp, CDS: 501-2144 (SEQ ID NO 185)
TCCAGTATGCCACACATTATGCCTTGCACACCTAAAGCACATATTTTCGTTATTTTTCAC
CACAATAGGTGGATCTCGAAAAGGATGGAAAATCAGGAAAAAGAAATGTTGAGAAAAAAA
TAAACCGATTCCCGTTTAGTTTTCTCCTATTTCCGTGTATATGCGTGGTTATTCGTTTTC
GAATCCTTTTATGAATGTCCGAGGAGGTGGTACAATCCGAAATAGACTAAAGAAAAGCGA
AAGCCGTGAGTTTGTTTGATGATAGATGACTCGCAGCTTTGTCATCAACGGGCCACCCTA
TTCGAAGAAGGGAATGGAAAACGGACTGGCGTAGTCAATAAGCGTCTTCATATCTTAGCA
TTGTTGAGAGATACATAGTGTACTCCATATCGTTCTTTTTTTTTGTATATATCAAGCCAC
ATATCCTGTTTCTTTAATCTTTTATACGCCGTAAGAATCGGGTACTGACATAAGTGTAAG
TAGCCGTACAGAGAACAAATATGACTAAATCGGTTGGTGATGAAGAGTCACAGTACATTG
AGGACCCTAGTTTTGCAGCAGCAGCTGCATTTACTGGCGGCAGGGACGGGGTTTCGTACA
GTAATCAGCGATTTGCTGAGGGTTCCGGCCATTCTTCTGACTTAGCAAAGTCATTAGAAG
ACTATCGGCCTCCTGATGAAAAGCCGTCCTCATTGTCATCTGTGGGGGAAGGTGGCGCTA
ATGAGGAAGAGAAGGGCGGTAACGACGGCGGTCCCTTGGCAAGAATTCAAACAGGGCTTT
TTTCTCCAAGACTGCGAAATCATAGGAAAAAGATTCTCTCGAAGTTTGTTTTGAACAACT
TCTTCATTGCTTGTGTGTGTGTATCGCTCATATCGATTTACTGGGGTGCCTGTTACGGAA
CAGATCGTTACTTTTTCAAAGTGAAAAATATTGTTGTATTGCAGGATGCGCCATCTAATA
CTTCAGTTCAATCTATTTCCGCGATCATACCCTCATTGTTAGCGTCTGTCCCCGGGACAT
GGCATATATACAACGCAACATCATTTCATAGGAAATTTGGTACGACGAACTCCACCGAAA
TTGACAGAAAGATAGTCGATTTAATTTACGATGAGAGATACTGGCTGGCGTTAAACGTTA
AACCTAATGCTACAGACACTTTGTATAATTCTTTGATTAGCCAAGACGCAAACTCGGAGT
TCAATTCATCAATTTTTTTTGAATCCGTGTTTGAAAGTGGTCGTGACCCATCGAGTGTTA
AATCGACCATTCTACCACTCATGCAACAATTGGAGGTCCGCCTTCAGAAATATTACGTCA
AGGAATATCTTCCCTCATTGATGAGCAACATCACTTCTAATGACAGAGATCTTAATATAA

ACATGGAGAACTGGGCGATTGCAGGACAGTTGTTGTTCACCTACAACGATTATCGTCCCT
TTGCTGATCGTATTCTAATGGCCCCTCTGCAGGTCGGTCTGATTTATTGTAATTTTGTTAA
CCGTTTTACAACTGTCATTATATGGTAAGTTGCACGGAGAAATGGCCAGAGTTCTGAAGC
CAAAGCATATTTTAATCTACAGGCTTCTAATTTCCTGGGCAACTTATTTTCTTCTTTCCA
TTGGATTCTGTACCGTATCTGCAATTTTTAGGATCGATTTCACCCCCGCCTTTGGCAGAG
GAGGATTCGTAGTATATTGGATGTCTACGTGGTTGGTAATGATGGCTGTTGGTGGTGCCA
ATGAAAACGTTCTCAGCTTAGTTATAGCTTACTGCCCTCCATACCTGAGTATTTGGTTGA
TGACGTGGATCATATTAAATATTTCTGCTTCATTCTACCCAATGGTTTTGAACAACGAAT
TTTACAGGTACGGCTACATAATGCCAATCCATAATGCCGTGGATATCTATAAAGTGATTT
TTTTGAATTTAACCAAAAGAAAAATGGGAAGAAATTACGGTATTCTCGTGGCATGGGTTG
CCCTCAATACATCCTTGATGCCATTTTGTATGAAGTTTGCAGGTAAAAAAATGCAAAAAA
ATGCTATGCAAGCAGCAGAAGCCGCTGTCGCAGCAGCTACCCAGCGTGCTAGCCGCCCGG
CAGAGGCCAATACTGATAAAAATAACAACCCGCCCGGAAATTAA

>YGR197C, 547 aa (SEQ ID NO 186)
MTKSVGDEESQYIEDPSFAAAAAFTGGRDGVSYSNQRFAEGSGHSSDLAKSLEDYRPPDE
KPSSLSSVGEGGANEEEKGGNDGGPLARIQTGLFSPRLRNHRKKILSKFVLNNFFIACVC
VSLISIYWGACYGTDRYFFKVKNIVVLQDAPSNTSVQSISAIIPSLLASVPGTWHIYNAT
SFHRKFGTTNSTEIDRKIVDLIYDERYWLALNVKPNATDTLYNSLISQDANSEFNSSIFF
ESVFESGRDPSSVKSTILPLMQQLEVRLQKYYVKEYLPSLMSNITSNDRDLNINMENWAI
AGQLLFTYNDYRPFADRILMAPLQVGLIYCILLTVLQLSLYGKLHGEMARVLKPKHILIY
RLLISWATYFLLSIGFCTVSAIFRIDFTPAFGRGGFVVYWMSTWLVMMAVGGANENVLSL
VIAYCPPYLSIWLMTWIILNISASFYPMVLNNEFYRYGYIMPIHNAVDIYKVIFLNLTKR
KMGRNYGILVAWVALNTSLMPFCMKFAGKKMQKNAMQAAEAAVAAATQRASRPAEANTDK
NNNPPGN

>YGR250C, 2846 bp, CDS: 501-2846 (SEQ ID NO 191)
TCTTGTGTACGTACGATGTTTCTCCCGCTGATCCGATTACTAGCCGAAGACGTAAAATTG
GCGCTTGATTCAATTTATGCCCTTCCCGGGAATAGTTGACCAAAGGGCAAAAAAATTCAG
TCGGAGATTCCCTATTGGGCGGAATTTAGTAGATCTCTTTCCGTGCATAACGCCTGCCCG
TTAGTCGTTATTTCACGTTAACATTTTCTTGGCCACTGCGCTATATAAATAAATACATAT
ATATATGTCAAGCACAATAAAGAAACTTCCCTTAAATATTGAATAAGTAAATAATAGTTG
AAAAGTGCCTTTTGTTCGAAGGATTAGAGTGTTCTTAATTTTAGTTCGTTCAACGGTCTC
AAAAAAAGTGTGAACAAGTAAAGCATAGCACACATCCCAAATTACAAGGCACCCTGATTA
AAAATCCAAAAATAAACCATAAGTTTTATTTTACTAAAAACATTATACGTGAAAGACAAA
CCGCATCAGAAGTTTCGAGGATGAATATTGCAGAAGAACCATCAGATGAAGTAATATCTA
GTGGCCCCGAGGATACAGATATCTGCAGCCAGCAGACATCAGCGAGCGCAGAAGCTGGAG
ACCAATCAATAAAAATTGAAAGGAAAACTTCCACTGGTCTTCAACTGGAACAATTGGCCA
ACACAAATTTATTAACCATAAGAATAAAATGGCAGTTACAAGAAGAAGAAGATGATCACT
GCAACTCTAGAATAACCGATCAAATAATGGACACAATACAGCACTACAAAGGTATCTCCG
TTAACAACTCTGATACAGAAACATATGAATTTCTTCCGGATACAAGGAGGTTACAGGTTC
TCGAACAAAATAAAGACATCTATCTTTACGAGCATGGAAGTCAAGAGTATGAGAAATCTT
ACAAAGATAACGAAGAGGAAGATGATTGGAGATACGATACCGTTTGCAAGCACAATTCA
AGTACCCCAAGTCATTAGAAAATGCATGTACAGATATCTCGGAATTACTCAAGAGCGAAC
CTATTGGTCAGCATATTGATAAATGGTCTATCGGTGTGAACAAGCATGCACTAACCTATC
CTGGAAATATTTTTGTCGGGGGAATAGCAAAGAGCCTTTCTATTGGTGAACTAAGTTTCT
TATTTTCAAAATATGGACCAATTTTATCAATGAAATTGATATATGATAAAACGAAAGGCG
AACCTAACGGATACGGGTTCATCTCCTACCCCTTGGGTTCTCAAGCTTCACTTTGCATCA
AGGAACTTAATGGAAGGACGGTAAATGGCTCCACACTATTTATCAACTATCACGTTGAGC
GAAAGGAGAGAGAAAGAATCCATTGGGACCATGTCAAAGAAAACAACAATGATGATAATT
TCAGGTGTCTCTTTATAGGCAACTTGCCTTATCACAATCCTGAAAAAGTAGAGACTTTGA
TTACACCTAAAGAAGTCATAGAAGTAATCAAGAAGGAGTTATCAAAAAAGTTTCCGGACT
TTGATATCATTTCATATTACTTTCCGAAGAGAAGTAATACAAGAAGCAGTAGTTCAGTAA
GTTTCAATGAGGAGGGGTCAGTAGAATCAAACAAATCTTCCAATAATACTAATGGAAATG
CCCAAGATGAAGATATGTTGAAGGGTTATGGTTTCATCAAGCTTATCAACCATGAACAAG
CACTAGCAGCCATCGAGACCTTCAATGGGTTCATGTGGCATGGAAACAGGCTCGTTGTTA

ATAAGGCGGTTCAACATAAAGTTTACAACAACCACAATAGCCATGACAGGCACCCTTCCA
TCAGTAACCACAATGATATGGAGGTTTTGGAATTTGCAAATAACCCAATGTATGATTACA
ATAATTATACATATGATAGATATTACTTCAACAATAATAAAAACGGGAACAGCAACGATA
CCTCCAATGTACGGTATTTTGATTCTGTAAGATCAACCCCTGTGGCAGAGAAAATGGATC
TGTTCTATCCTCAAAGGGAATCTTTCAGTGAAGGTCGTGGTCAACGTGTGCCTAGATTCA
TGGGCAACAAGTTTGACATGTACCAGTACCCATCAACTTCTTACAGCTTACCTATACCAA
TGAGTAATCAGCAAGAATCAAACCTATATGTCAAGCACATCCCTCTTTCTTGGACAGATG
AAGATTTATATGATTTCTACAAATCTTTCGGTGAAATAATCAGCGTTAAGGTCATTACTG
TTGGGGGTAGTAAGAACAAGTATCGTCAACAATCGAATGATAGCTCATCAGATAATGATC
TGCCAGTGGGATCATCAAGAGGTATGGTTTTGTTTCTTTTGAAAGCCCATTAGATGCTG
CTAAGGCAATTTTGAATACAGACGGGTATCAAGTGAGCAAAGATCAAGTGTTATCTGTTT
CTTTCGCTCAGAAACGTGGTAATTTATCTTCAAGTGATGATGATGATCAATCCCAAACTG
ATAACTCATCAAAGTTCCAAAATTTTCAGCCACATAATGATTATCATAAGGCTTATCCAA
CAAAGTATAATAAGAAATTTATCAATGCCTTGATGACTCAGAACCAATCGCAACAGCAAG
TCTCGAGGGAAAATTATTTCATACCACTGCAGTACCCTAATACCAACACAAAGCCCGTGA
ACAGTTACAACTTAATAAGTGCAAACCAAAATAACGCTAACTGGATGATGCCAATGTTCC
CATCATTTGGGTTTATTCCACAGGTGCCGCCAGTGCCCTATATAATACCTCCGCAGAATC
CTGCAGCAAATCATATTCCTATAATGGCAAACGGTAGTAATGAAGAGGAAGAATTTTCTA
GTGGTGATTATTCTATGGACTACTAG

>YGR250C, 781 aa (SEQ ID NO 192)
MNIAEEPSDEVISSGPEDTDICSQQTSASAEAGDQSIKIERKTSTGLQLEQLANTNLLTI
RIKWQLQEEEDDHCNSRITDQIMDTIQHYKGISVNNSDTETYEFLPDTRRLQVLEQNKDI
YLYEHGSQEYEKSYKDNEEEDDWRYDTVLQAQFKYPKSLENACTDISELLKSEPIGQHID
KWSIGVNKHALTYPGNIFVGGIAKSLSIGELSFLFSKYGPILSMKLIYDKTKGEPNGYGF
ISYPLGSQASLCIKELNGRTVNGSTLFINYHVERKERERIHWDHVKENNNDDNFRCLFIG
NLPYHNPEKVETLITPKEVIEVIKKELSKKFPDFDIISYYFPKRSNTRSSSSVSFNEEGS
VESNKSSNNTNGNAQDEDMLKGYGFIKLINHEQALAAIETFNGFMWHGNRLVVNKAVQHK
VYNNHNSHDRHPSISNHNDMEVLEFANNPMYDYNNYTYDRYYFNNNKNGNSNDTSNVRYF
DSVRSTPVAEKMDLFYPQRESFSEGRGQRVPRFMGNKFDMYQYPSTSYSLPIPMSNQQES
NLYVKHIPLSWTDEDLYDFYKSFGEIISVKVITVGGSKNKYRQQSNDSSSDNDLPVGSSR
GYGFVSFESPLDAAKAILNTDGYQVSKDQVLSVSFAQKRGNLSSSDDDDQSQTDNSSKFQ
NFQPHNDYHKAYPTKYNKKFINALMTQNQSQQQVSRENYFIPLQYPNTNTKPVNSYNLIS
ANQNNANWMMPMFPSFGFIPQVPVPVYIIPPQNPAANHIPIMANGSNEEEEFSSGDYSMD
Y

>YHR001W-A, 797 bp, exon1: 501-506, intron1: 507-569, exon2: 570-797 (SEQ ID NO 195)
TTCTATTCCGGCTTATAAAAAGCATGGAATCCAAAAGAATTAGGCTTCTCATTCTATTTT
AATTATACTAGTACGATTTCTCACTCTGTAATTTAATATCAGTGTAATATGCACCTAGTT
ATGGGTAGTTTTTGCTAACGTTACGAGCCGCGAAACTGTCCTCAATCTTCACCACTACCT
CTAATGACTGAAGAATGCTATGCGATATAACGCTGTCGCACTTTGAATATATACTTATAT
TTACATAGTTTTCAAGTGCGTATTACTATTGCAAAGTAGTATTTTGTCACGTGATTTTGA
TCCAATTAAAACTAAATATGGTTCAACCCGTTGTTTCCGCATCAAAAAACCATACCATTT
ATCAAGGGGACGGGATATATCACATAACAGTTTGAATGCATAATTTGTTATAGATATCTT
CTGGAATAATCTTCACAGCAAAAGCGCAAGTCGAATAATATATCGATAAATACAATCCAT
AAGACTTAAAACTAACCTCAATGGCGGTAAGTATCCTATCATATTATGTGAGCTAGAACC
GAATTAGTATACTAACATTTATAATACAGTACACTTCTCATCTGTCTTCAAAAACTGGTC
TACATTTCGGTAGACTTTCTTTAAGAAGTTTAACAGCTTATGCTCCGAATTTAATGTTAT
GGGGTGGTGCTAGCATGCTTGGGCTATTTGTATTCACAGAAGGATGGCCTAAGTTTCAAG
ATACGCTATACAAAAAGATTCCGTTGTTAGGACCTACATTGGAAGATCATACTCCACCAG
AAGATAAACCTAATTGA

>YHR001W-A, 77 aa (SEQ ID NO 196)
MAYTSHLSSKTGLHFGRLSLRSLTAYAPNLMLWGGASMLGLFVFTEGWPKFQDTLYKKIP
LLGPTLEDHTPPEDKPN

>YJL142C, 893 bp, CDS: 501-893 (SEQ ID NO 225)
TGCTGAATTATTTTTGGGTATACCGATCTTCCCAGGCGCTTCTGAATATAACCAATTAAC
AAGAATAATAGACACGCTTGGATATCCTCCATCGTGGATGATAGATATGGGTAAAAACTC
TGGAAAATTTATGAAGAAATTGGCACCAGAAGAAAGTTCTTCTTCTACACAAAAGCATCG
TATGAAAACTATTGAAGAGTTTTGCAGAGAATACAATATAGTGGAAAAGCCCAGTAAACA
ATATTTTAAGTGGAGAAAGTTACCAGATATTATTAGAAACTACAGGTATCCTAAAAGCAT
ACAGAACTCCCAAGAACTTATCGACCAAGAAATGCAGAATAGGGAGTGTTTGATCCACTT
TTTAGGCGGTGTGCTAAATTTGAACCCGTTAGAAAGATGGACACCACAACAAGCTATGCT
ACACCCCTTCATAACAAAGCAGGAGTTTACAGGTGAGTGGTTTCCTCCAGGATCGTCTTT
ACCGGGTCCTTCAGAAAAACATGACGATGCAAAAGGCCAGCAAAGTGAATATGGAAGTGC
GAACGACTCTAGTAACAATGCAGGCCACAACTATGTCTATAATCCTAGCTCTGCCACTGG
TGGTGCTGATAGCGTCGACATTGGTGCTATCAGTAAAAGGAAGGAGAATACATCTGGCGA
CATCTCCAATAATTTTGCTGTTACTCATTCTGTTCAAGAAGGCCAACAAGCGCGTTCAA
TAAACTTCACATTGTCGAAGAATAAATCGTTATTTGTCTGACTTTTCTTAACTACCCAT
TTCATTTTATTACGGCTTGGTGCCATAATGATATACTAAATAAATATGAATTTTGCCTTT
TCTTAATTTTCCTTATACGTATAGTCATTACAATTAATAAAGTAACATTATAA

>YJL142C, 130 aa (SEQ ID NO 226)
MTMQKASKVNMEVRTTLVTMQATTMSIILALPLVVLIASTLVLSVKGRRIHLATSPIILL
LLILFKKGQQARSINFTLSKNKSLFCLTFLNYPFHFITAWCHNDILNKYEFCLFLIFLIR
IVITINKVTL

>YJL144W, 815 bp, CDS: 501-815 (SEQ ID NO 227)
AGAAAGAAGTTCGTGGTATTAACCGACGGCAGCAAGTTGGGTCAATACTTGAAGGATTGC
CCATATGAAGGGTATGGCGGGAAAGATAAGAAGAACAATCTGACCAAGCAAAATGTCACA
AATGTCCATCCAACAGAATACGGCCTTTACATTTTACAAAAACAAATCATCGAGGACGTT
GAGTGATTTGTTGGCATGATCTAATAATAGTCTCTATATAAACCCTATAATAATTTCTTT
ATTTTTGCCTTATATTCAGGTAAATCACCATCTAACTGTATTATCTCTCACGTATCTTCA
CTTATATGGCTCAGAAAACACCGTACGAAACGAAGGGGCTGCGAAAATGTTTCTAGAAGG
TAATGGCAATAATAGGGATACAGATCGATCAGATCCGCCTATATAAAAGACAACGCACCG
AAGGTGAACAAGATCGCAGATAAAGGTATTTACAAGGGAAAAAAGTCAGCAAAAACAAGA
GATAAGATAACAAGAAGAAGATGTTAAGGAGGGAAACTTCAACAATATACAGGACACACA
AAAAAAGCAACAGTAGTATACTCAGGAGCCAGCGGGACCAGACTAGAGTGGATTCCTTGG
TAGAGGAGTCTCCCATGGGCGATTTCGGGATCAATAACCAGCCTACACAGCCTGGCGTGA
TATACTACTTTGTAGAGCTGACTAATTTAGGCATACAGGAAAACACAAGCAGTAATAATA
ACAACAACAATAATCATGGTGACGATGAAAACGGCAGTCGATACGGCCACGGCAGCAGTC
TGGGTGGAGACGTTCACTCTCGCCGTTGTTCATGA

>YJL144W, 104 aa (SEQ ID NO 228)
MLRRETSTIYRTHKKSNSSILRSQRDQTRVDSLVEESPMGDFGINNQPTQPGVIYYFVEL
TNLGIQENTSSNNNNNNNHGDDENGSRYGHGSSLGGDVHSRRCS

>YJL166W, 785 bp, CDS: 501-785 (SEQ ID NO 231)
TGAACAGCTATACCACGAATATGAAGAGTCTATTGCCAAGGATTTGAAGGCCAAAATTTC
TCAGGTCGATGAGTCTCGTGGCTTCAAAGCTGATGTCTTAACTGCGTTCTTGAACAAAGT
TTACAAGAGAAGCAAATAGAACTAACGCTAATCGATAAAACATTAGATTTCAAACTAGAT
AAGGACCATGTATAAGAACTATATACTTCCAATATAATATAGTATAAGCTTTAAGATAGT
ATCTCTCGATCTACCGTTCCACGTGACTAGTCCAAGGATTTTTTTTAAGCCAATGAAAAT
GAAGAAATGCGTGATCGGAAATTACGGGTAGTACGAGAAGGAAACTTGAGCCACCCCCCA
AATTTTATTCATATAATAATAGGAAAAGCAACGACCTCATCTCTCGAACATTGTTTACTT
GAGCAAGTCCGATTAAGAGTAAGTTGTCGTACGTTAAATACAAATAATCAACAAAACACT
ACACAAAAACTTCTACGATAATGGGTCCTCCAAGCGGTAAAACTTACATGGGATGGTGGG
GTCACATGGGTGGTCCAAAGCAAAAAGGTATAACCTCATATGCTGTGTCTCCATATGCTC
AAAAGCCATTACAAGGTATTTTCCATAACGCTGTATTCAATAGTTTTAGAAGATTTAAGT
CTCAATTTCTATATGTATTAATACCTGCGGGAATTTATTGGTACTGGTGGAAGAACGGTA
ACGAGTATAATGAATTTCTGTACAGCAAAGCTGGTAGAGAAGAGCTGGAAAGAGTTAATG